GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2004, 15:11:01; Search time 56 Seconds (without alignments) 427.709 Million cell updates/sec Run on:

US-09-598-982-21 1393 1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP 249 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	yptase (	tryptase (EC 3.4.2	(EC	(EC 3	mast cell proteina	_	l trypta	tryptase (EC 3.4.2	(EC 3.4	_	mast cell proteina		prostasin (EC 3.4.	coagulation factor	plasma kallikrein	plasmin (EC 3.4.21	plasma kallikrein	plasmin (EC 3.4.21	kall	pancreatic elastas	chymotrypsin (EC 3	m			pancreatic elastas	ט	plasmin (EC 3.4.21	chymotrypsin (EC 3	pancreatic elastas
SUMMARIES	AI.	B35863	A35863	C35863	A45754	A38654	A32410	856160	A47246	JC4171	S68702	I48685	B32410	A57014	KFHU1	КОНИР	A61545	KOMSPL	PLBO	KORTPL	ELRT2	KYBOB	B61545	T30337	B26823	A25528	PLHU	B30848	A21195	ELPG
	DB	7	ď	7	N	7	7	71	~	N	~	7	0	-	Н	Н	7	Н	-	Н	Н	Н	~	7	~	C1	Н	7	~	-
	Length	275	275	275	274	276	275	270	273	274	237	230	269	343	625	638	455	638	812	638	271	245	460	N	269	271	810	810	263	266
₩ .	Match	98.2	97.8	96.1	88.5	78.3	77.3	7	75.7	75.4	72.1	57.9	49.1		33.5	32.4	32.2	32.1	32.1		31.9		٠		ä	30.9	٠		ö	30.7
	Score	1368	1363	1339	1232.5	1091	1077	1075	1054	1051	1005	807	684.5	512	467	451	448	447	446.5	445	444.5	4	441	43	9	430.5	429	428	427	427
t	No.	-	7	m	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

chymotrypsin (EC 3	chymotrypsin (EC 3	plasmin (EC 3.4.21	serine proteinease	chymotrypsin (EC 3	plasma hyaluronan-	plasmin (EC 3.4.21	trypsin (EC 3.4.21	trypsin (EC 3.4.21	chymotrypsin-like	testicular serine	pancreatic elastas	pancreatic elastas	probable pancreati	apolipoprotein(a)	trypsin (EC 3.4.21
A31299	KYRTB	PLMS	A47547	KYBOA	JC5878	PLPG	B25528	TRRT2	138136	JE0104	C26823	S70439	A56615	A32869	TRRT1
N	Н	-	Н	Н	N	Н	7	Н	7	7	7	4	4	7	Н
263	63	812	786	245	558	790	246	246	264	367	269	258	267	1420	246
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		30.2	30.2	30.1	30.1	30.1	29.9	29.8	29.8	29.7	29.6	29.6	29.6	29.5	29.4
		30.2	_	419 30.1			416.5 29.9					412 29.6	412 29.6	411 29.5	409.5 29.4

## ALIGNMENTS

activities as a serious as a se	C; Genetics: A; Gene: GDB:17FS1 A; Gene: GDB:17FS1 A; Cross-ferences: GDB:125890; OMIM:191080 A; Map position: 16pter-16qter C; Superfamily: trypsin; trypsin; homology C; Keywords: hydrolase; serine proteinase; zymogen C; Keywords: hydrolase; serine proteinase; zymogen F; 1-21/Domain: activation peptide #status predicted <act> F; 22-30/Domain: activation peptide #status predicted <act> F; 31-27/Pomain: tryptase I #status predicted <act> F; 31-27/Pomain: tryptase I #status predicted <act> F; 31-27/Active Site: His, Asp, Ser #status predicted Query Match Best Local Similarity 99.6%; Score 1368; Dred. No. 1.1e-119; Match Conservation of the mismatch of the mismatch</act></act></act></act>
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DE STREET	Db 91 REQHLYYQUOLLPVSRITUHDQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFP 150  Qy 125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRLYBDML 184
Db 31 IVGGGRAPRSKWPRQVSLRVHGPYTANGIGADIALIZEERPWWYSTRP9124  Db 91 REQUIYYODOLLVVSRIIVHOPYTANGIGADIALIZEERPWWSSTWPT12P120  OY 125 PORMCHWTGWDDLVSRIIVHOPYTANGIGADIALIZEERPWWSSWHYTLPRDSTTP 150  OY 125 PORMCHWTGWDDLVSRIIVHOPYTANGIGADIALIZEERPWWSSWHYTLPRDDVL184  Db 121 RAGHLYYDODLLVSRIIVHOPYTANGIGADIALIZEERPWWSSWHYTLPRDDVL184  Db 121 RAGHLYYDODLLVSRIIVHOPYTANGIGADIALIZEERPWWSSWHYTLPRDDVL184  Db 121 CAGNTREDSCQDSGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  Db 211 CAGNTREDSCQDSGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  DD 245 VDKKP 249  DD 245 VDKKP 275  REBULT 2  ANGEGGE BD 3-4.21,59) I DREGUEGC - human  C.DARCH CAGNTREDSCQDSGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  DD 271 VPKKP 275  RESULT 2  ANGEGGE BD 3-4.21,59) I DREGUEGC - human  C.DARCH CAGNTREDSCQDSGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  DD 245 VDKKP 275  ANGEGGE BD 3-4.21,590 I DREGUEGC - human  C.DARCH CAGNTREDSCQDSGGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  ANGEGGE BD 3-4.21,590 I DREGUEGC - human  C.DARCH CAGNTREDSCGDSGGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  ANGEGGE BD 3-4.21,590 I DREGUEGC - human  C.DARCH CAGNTREDSCGDSGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  ANGEGGE BD 3-4.21,590 I DREGUEGC - human  C.DARCH CAGNTREDSCGDSGGPLVCKNATWLQAGVVSWGGGCAQPRRECHTRVTYLDWHHNY 244  ANGEGGE BD 3-4.21,590 I DREGUEGC - HUMAN  A.REGEGGE BD 3-4.21,590 I WID:9021647; PRID:210193  A.ACGGGGG CON ANGEGGE BD 3-4.21,74,74,48,77,45,68,77,50 GBUT>  A.REGGEGGE BD 3-4.21,74,74,48,77,45,48,77,50 GBUT>  A.REGGEGGE BD 3-4.21,74,74,48,77,45,48,77,50 GBUT>  A.REGGEGGE BD 3-4.21,74,74,74,48,77,74,74,74,74,74,74,74,74,74,74,74,74,	F;22-30/Domain: activation peptide #status predicted <act> F;31-275/Product: tryptase I #status experimental <mat> F;31-267/Domain: trypsin homology <try> F;31-267/Domain: trypsin homology <try> F;74,121,224/Active site: His, Asp, Ser #status predicted  Ouery Match  Ouery Match</try></try></mat></act>

Fri Jul

tryptase (BC 3.4.21.59) alpha precursor - human

C; Species: Homo sapiens (man)

A; Molecule type: mRNA A; Residues: 1-274 <MIL>

A; Accession: A45754

m

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A,Molecule type: mRNA
A,Residues: 1-276 <RE2>
A,Eresidues: 1-276 <RE2>
A,Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
A,Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
B,Till: Different Acad. Sci. U.S.A. 87, 3230-3234, 1990
A,Till: Different mouse mast cell populations express various combinations of at least s
A,Reference number: A35646; MUID:90222202; PMID:2326280
                                                                                                                                                                                                                                                                                                             A, Molecule type: protein
A, Residues: 32-54 <RB3-
A; Residues: 32-54 <RB3-
R; Huang, A. Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson,
Scand. J. Immunol. 38, 359-367, 1993
A; Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 1986
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural
A;Reference number: A32410; MUID:89352460; PMID:2504277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-275 <VAN>
A;Cross_references: GB:M24664; NID:g163982; PIDN:AAA30854.1; PID:g163983; GB:J02862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 REQYLYYGDQLLSLNRIVVHPHYYTAEGGADVALLELBVPVNVSTHIHPISLPPASETFP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CAGNTREDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aintrons: 24/1; 79/2; 168/1; 222/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; servine proteinase; zymogen
F;1-21/Domain: aignal sequence #status predicted <SIG>
F;22-31/Domain: activation peptide #status predicted <ACT>
F;22-276/Product: mast cell proteinase 6 #status experimental <AMI>
F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: 159478; MUID:94023807; PMID:8210998
A;Accession: 159478
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C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.3%; Score 1091; DB 2; 78.2%; Pred. No. 6.6e-94; iive 19; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tryptase (EC 3.4.21.59) precursor - dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-276 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 VPK 247
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R;Vanderslice, P.; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A32410
A;Accession: B38654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
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C;Date: 21-Feb-1992 #sequence revision 17-Feb-1994 #text_change 22-Jun-1999
C;Date: 21-Feb-1992 #sequence revision 17-Feb-1994 #text_change 22-Jun-1999
C;Accession: A38654; B38654; D5546; I59478
S;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by pr
A;Reference number: A38654; MUID:91139682; PMID:1995638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pro C,Superfamily: trypsin; trypsin homology C,Keywords: hydrolase; serine proteinase; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: GB:M30038
R, Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human tryptase.
A;Reference number: A37193; MUID:90369005; PMID:2203827
                                                                                                                                                      C;Date: 03-Jun-1993 #sequence revision 03-Jun-1993 #text_change 08-Sep-1997 C;Accession: A4554; B37193 **
R;Miller, J.S.; Westlin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1988 A;Title: Cloning and characterization of complementary DNA for human tryptase. A;Reference number: A45754; MUID:90009311; PMID:2677049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 SGTHLYYQDQLLPVSRIMVHPQFYIIQTGADIALLELEEPVNISSRVHTVMLPPASETFP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGMPCWVIGWGDVDNDEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDML 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 CAGNSQRDSCKGDSGGPLVCKVNGTWLQAGVVSWDEGCAQPNRPGIYTRVTYYLDWIHHY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGNTRADSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
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F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-30/Domain: activation peptide #status predicted <ACT>
F.312-34/Product: tryptase I #status predicted <ART>
F.31-26/Domain: tryptasin homology <TRY>
F.31-26/Domain: trypsin homology <TRY>
F.74,120,223/Active site: His, Asp, Ser #status predicted

A; Cross-references: GB:M30038

A; Molecule type: mRNA A; Residues: 1-274 <MI2>

A; Accession: B37193

88.5%; Score 1232.5; DB 2 89.8%; Pred. No. 4.4e-107; ive 7; Mismatches 17;

220; Conservative

65

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150 185

125

Similarity

Query Match Best Local {

Matches

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A;Cross-references: GB:MS7625; NID:g200506; PIDN:AAA39987.1; PID:g200507
A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37
s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A; Molecule type: DNA
A; Residues: 1-276 < REY>
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A; Accession: A38654

mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse

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R,McNeil, H.P.; Reymolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.; E Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A,Title: Isolation, characterization, and transcription of the gene encoding mouse mast c A,Reference number: A47246; MUID:93087489; PMID:1454796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tryptase (EC 3.4.21.59) precursor - rat
N;Alternate names: mast cell tryptase
N;Alternate names: mast cell tryptase
S;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4171
R;Ide, H.; Itch, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.; Osada, Y.; Na Biochem. 118, 210-215, 1995
A;Title: CDNA sequencing and expression of rat mast cell tryptase.
A;Reference number: JC4171; MUID:96015171; PMID:8537314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Residues: 1-274 < IDB>
A,Cross-references: DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g556556
C;Comment: This enzyme is basically specific for a connective tissue mast cell, it is uperinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                               tryptase (EC 3.4.21.59) 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Superfamily: trypsin; trypsin homology
C, Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
C, Keywords: glycoprotein; hydrolase; mast cells
F, 20-29/Domain: activation peptide #status predicted <ACT>
F, 30-274/Product: mast cell tryptase #status predicted <AMT>
F, 30-266/Domain: trypsin homology <TRY>
F, 31-20, 223/Active site: His, Asp, Ser #status predicted
F, 31-120, active site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 IVGGÓBAHGNKWPWÓVSLRANDTYWMHFCGGSLIHPOWVLTAAHCVGPDVADPNKVRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IVGGQBAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAAACVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                      75.4%; Score 1051; DB 2; Length 274; 75.8%; Pred. No. 3.4e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.7%; Score 1054; DB 2; Length 273; 76.5%; Pred. No. 1.8e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.7%; Score 105%; U-Best Local Similarity 76.5%; Pred. No. 1.8e-Matches 186; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                        A; Molecule type: nucleic acid
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 VPK 271
                                                                                                                                                                                                                                                                   A; Accession: A47246
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 VPK 247
                                                                                                                                  C; Accession: A47246
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C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: S56160
R;Murakumo, Y: 1de, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.;
Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones
A;Reference number: S56160; MUID:95366971; PMID:7639711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TGTPCWVTGWGDVHSGTPLPPPFPLKQVKVPIVENSMCDVQYHLGLSTGDGVKIVREDML 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGNSKSDSCQGDSGGPLVCRVRGVWLQAGVVSWGEGCAQPNRPGIYTRVAYYLDWIHQY 270
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                                                                                                                                                                                                                                                                                                                                                                                  CAGNTRRDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                                                                                                                                                                                                                                                                                 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
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                                                                                                                                                                                                                                            5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 CAGNEGHDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCALPNRPGIYTRVTYYLDWIHRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
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C;Superfamily: trypsin; trypsin homology
F;26-262/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                         IVGGREAPGSKWPWOVSLRLKGOYWRHICGGSLIHPOWVLTAAHCVGPNVVCPEEIRVQL
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                                                                                                                                  Score 1077; DB 2; Length 275; Pred. No. 1.3e-92;
                                                                                                                                                                                       35; Indels
F;22-30/Domain: activation peptide #status predicted <ACT>
873-275/Product: tryptase #status predicted <MAT>
F;31-267/Domain: tryppsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S56160
mast cell tryptase precursor - Mongolian jird
                                                                                                                             77.38;
                                                                                                                                                                                       Matches 189; Conservative
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A;Molecule type: mRNA
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Best Local S
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R;Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4184-4155, 1989
A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural &
A;Reference number: A32410; MUID:89352460; PMID:2504277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 PSLIVPPGMLCWVTGWGDIADHTPLPPPYHLQEVPIVGNRECNCHYQ--TILEQDDBV 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mastocytoma proteinase (BC 3.4.21.-) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 10-Sep-1997
   R;Huang, R.; Hellman, L.
Immunogenetics 40, 397-414, 1994
A;Title: Genes for mast-cell serine protease and their molecular evolution.
A;Reference number: 148684; MUID:95048582; PMID:7959952
A;Accession: I48685
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X78542; NID:g468809; PIDN:CAA55288.1; PID:g468810 C.S. Superfamily: trypsin, trypsin homology C;Superfamily: trypsin; serine proteinase C;Keywords: hydrolase; serine proteinase F;32-230/Domain: trypsin homology #status atypical <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 IVGGHEASESKWPWQVSLRFKLNYWIHFCGGSLIHPQWVLTAAHCVGPHIKSPQLFRVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
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C; Keywords: hydrolase; serine proteinase
F)-19/Domain: signal sequence #status predicted <SIG>
F;0-259/Product: mastocytoma proteinase #status predicted
F;20-259/Domain: trypsin homology <TRY>
F;66,116,217/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
49.1%; Score 684.5; DB 2;
Best Local Similarity 52.6%; Pred. No. 4.4e-56;
Matches 132; Conservative 32; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.9%; Score 807; DB 2; Best Local Similarity 74.3%; Pred. No. 1.4e-67; Matches 142; Conservative 17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGNTREDSCQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGNTREDSCO 222
                                                                                                                                                                                                                 A; Residues: 1-230 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: B32410
A; Molecule type: mRNA
A; Residues: 1-269 < VAN>
                                                                                                                                                                                     A; Molecule type: mRNA
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                                                                                                                                                                                                                 90 REQYLYYADQLLTVNRTVVHPHYYTVEDGADIALLELEIPVNVSTHIHPISLPPASETFP 149
                                                                                                                                                                                                                                                                                                                                 150 SGTSCWVIGWGDIDSDEPLLEPPYPLKQVKVPIVENSLCDRKYHTGLYTGDDVPIVQDGML 209
                                                                                                                                                                                                                                                                                                        184
                                                                                                                                                                                                                                                                                                                                                                                                                   185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTXYLDWIHHY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 CAGNTRSDSCQGDSGGPLVCKVKGTWLQAGVVSWGEGCAFANRPGIYTRVTYYLDWIHRY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S68702; S68676
R;Pallaoro, M.; Gambacurta, A.; Fiorucci, L.; Mignogna, G.; Barra, D.; Ascoli, Bur. J. Biochem. 237, 100-105, 1996
A;Title: cDNA cloning and primary structure of tryptase from bovine mast cells A;Reference number: S68676; MUID:96203914; PMID:8620861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLLPVSRIIVHPOFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                      89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOWPWQVSLRVSRRYWRHHCGGSLIHPQWVLTAAHCVGPEVHGPSYFRVQLREQHLYYQD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S68702
A;Molecule type: mRNA
A;Residues: 1-237 <PAL>
A;Cross-references: EMBL:X94982; NID:g1332446; PIDN:CAA64438.1; PID:g1332447
A;Accession: S68676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C;Accession: I48685; 843172
                                                                                                                                                                           REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP
                                                        5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                                   30 IVGGREASESKWPWQVSLRFKFSFWMHFCGGSLIHPQWVLTAAHCVGLHIKSPELFRVQL
                                                                                                                                                                                                                                                                                               125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP 249
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 'IVGGQEAP',1-8;61-74;90-97;126-148;162-190;208-222;227-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apperfamily: trypsin; trypsin homology
C; Superfamily: trypsin; hydrolase; serine proteinase; zymogen
C; Keywords: glycoprotein; hydrolase; serine proteinase; zymogen
E;1-229/Domain: trypsin homology (fragment) <TRY>
E;36,83,177/Active site: His, Asp, Ser #starus predicted
E;94,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQGDSGGPLVCKVNGTWLQAGVVSWGDGCAKPNRPGIYTRVTSYLDWIHQYVPQGP
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38; Indels
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tryptase (EC 3.4.21.59) - bovine (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 75.4 les 178; Conservative
185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 VPKK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 VPQR 273
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Matches
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A;Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tar A;Reference number: A00920; MUID:86243360; PMID:3636155
A;Accession: A00920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 28-33;35-49,'X',51-55,'X',57-63;70-75,'X',77-79;107-109,'X',111-112;132-139;'
Z50-282, X',284;287-37;313-316,'X',318-319;320-326;'X',328-330;'X',347-349;373,'X',375;
C; Comment: The proenzyme consists of two identical chains linked by one or more disulfide he active site, and a heavy chain, which associates with high molecular weight (HWW) kini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 4q35-4q35
A;Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the proteolytic activation of coagulation factor IX
A; Pathway: blood coagulation intrinsic pathway
C; Superfamily: coagulation factor XI; trypsin homology
C; Superfamily: coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydrol
F; 1-18/Domain: signal sequence #status predicted <SIGS
F; 19-387/Product: coagulation factor XIa heavy chain #status experimental <HCH>
F; 19-108/Domain: apple repeat <API>
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F;29/Disulfide bonds: interchain #status experimental
F;46-76,50-56,110-193,136-165,140-146,200-283,205-255,230-236,291-374,317-346,321-327,386
F;90,126,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;339/Disulfide bonds: interchain #status predicted
F;387-384/Cleavage site: Arg-IIE (coaquidation factor XIIa) #status experimental
F;431,480,575/Active site: His, Asp, Ser #status predicted
F;491/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Location of the disulfide bonds in human coagulation factor XI: the presence A;Reference number: A37940; MUID:91152017; PMID:1998667
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                                                  coagulation factor XIa (BC 3.4.21.27) precursor [validated] - human N,Alternate names: antihemophilic factor C; plasma thromboplastin antecedent C;Specias: Homo sapiens (man) C;Date: 13-Aug-1966 #sequence revision 26-May-1994 #text_change 08-Dec-2000 C;Date: 13-Aug-1966 #sequence revision 26-May-1994 #text_change 08-Dec-2000 C;Accession: A27431; A00920; A37940 B;Askal, R; Davie, E.W.; Chung, D.W. Biochemistry 26, 7221-7228, 1997 A;Title: Organization of the gene for human factor XI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2056-2060, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M18295
A;Note: the sequence shown follows the authors' translation
R;Fujikawa, K; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:119891; OMIM:264900
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A; Residues: 1-625 <FUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-625 <ASA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A37940
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Best Local S
Matches 99
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A, Note: parts of this sequence were determined by protein sequencing
R; Yu, J.X.; Chao, L; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A, Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification, A, Reference number: A54866; MUID: 94308140; PMID: 8034638
                                                                                                                                                                                                                                                                                                                                               prostasin (EC 3.4.21.-) precursor - human
C;Specias: Home sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
C;Accession: A57014; A54866
C;Accession: A57014; A54866
B;Yu, U.X.; Chao, L.; Chao, L.; Chao, L.;
Will Biol. Chem. 270, 11483-11489, 1995
A;Title: Molecular cloning, tissue-specific expression, and cellular localization of Pa;Recession: A57014; MUD:95286644; PMID:7768952
A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VRDDMLCAGNTR--RDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 VQEDMVCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: GDB:PRSS8
A;Cenes: GDB:676446; OMIM:600823
A;Cenes: references: GDB:676446; OMIM:600823
A;Map position: 16p1.2-16p1.2
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F;1-32-140-0main: signal sequence #status predicted <NAT>
F;33-44/Domain: prostasin light chain #status predicted <CHL>
F;45-343/Domain: prostasin light chain #status predicted <CHL>
F;45-343/Domain: prostasin light chain #status predicted <CHL>
F;45-343/Domain: prostasin light chain #status predicted <CHL>
2 EKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QARITGGSSAVAGOWPWOVSITYEG---VHVCGGSLVSEOWVLSAAHCF-PSEHHKEAYE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;45-281/Domain: trypsin homology <TRY>
F;323-341/Domain: transmembrane #status predicted <TWM1>
F;37-154.70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted F;85,134,238/Active site: His, Asp, <Estatus predicted F;85,134,238/Active site: His, Asp, <Estatus predicted F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:L41351; NID:9862304; PIDN:AAC41759.1; PID:9862305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%; Score 512; DB 1;
41.4%; Pred. No. 6.7e-40;
iive 39; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 YLDWIHHYV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 YASWIQSKV 285
                                                                                                                                                                              257 SWIHOHIPLSP
                                                                                                             239 DWIHHYVPKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 45-64 < YUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-343 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A54866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
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448 YSGILNLSDIT 120 SETFPEGMECW 508 GDTSTITNCW 174 DDVRIVRDDME 174 DDVRIVRDDME 175 QDYRITQ-RWY 232 TRVTYXLDWI 1	Db 612 TkVAEYADVA 621  Search completed: July 22, 2004, 15:26:16  Job time: 57 secs
QY         118 PASETPPPGMPCWVTGWGDVDNDERLPPFPLKQVKVPIMENHICDAKYHLGAY 171           Db         503 SKGDRNVIXTDCWVTGWGYRRLRDKIQNTLQKAKIPLVTNEECQKRYRGHKI 554           QY         172 TGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG 229           Db         555 THKMICAGYREGGKDACKGDSGGPLSCKHNEVWHLVGITSWGEGCAQRERPG 606           QY         230 IYTRVTXYLDMI 241           Db         607 VYTNVVEYVDMI 618	PERSONT 15  PAGENE PAINTEEN (EP. 3.4.11.34) precursor - human  Nathernate homes: Kinjohan pages presabliktein  C.Species Enco. septean. Genin pages presabliktein  S. A. 1912. Hand planama presabliktein, a A.; Davie, E.W.  Biochemistry 25, 210-2477, 1939  C.Accession: A00921  A. 1912. Hand planama presabliktein, B.A.; Davie, E.W.  A. 1912. Hand planama presabliktein  A. 1912. Hand planama presabliktein  A. 1912. Location of the disabliktein  A.

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256-565-60

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> 0 < | Intelligenetics > 0 < | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 | | 0 |
```

GENALIGN - Multiple Sequence Alignment Program Release 5.4

Fri 23 Jul 104 8:15:25-PDT

Solution Parameters:

```
Amino Alphabet = Identity
Compress = 0ff
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
DELetion-weight = 5.00
LEngth-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
SPread-factor = 50
```

Clustered order of selected sequences:

```
16. US-09-598-982-43 (1-249)
15. US-09-598-982-41 (1-249)
7. US-09-598-982-25 (1-249)
8. US-09-598-982-27 (1-249)
5. US-09-598-982-21 (1-249)
6. US-09-598-982-23 (1-249)
14. US-09-598-982-39 (1-249)
13. US-09-598-982-39 (1-249)
14. US-09-598-982-37 (1-249)
```

Region Alignment: (listed in Clustered order)

1 LEKRIVGGGAAPRSKWPWQVSLRVHGPVWMHFCGGSLIHPQWVLTAAHCVGEDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCCGGSLIHPWWVLTAAHCVGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWWHFCCGSLIHPQWVLTAAHCVGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCCGGSLIHPQWVLTAAHCVGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWWHPCCGSLTHPQWVLTAAHCYGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCCGSLIHPQWVLTAAHCVGPDVKDLAALR	1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLHFPQWVLTAAaCYGPDVXDLAALR	1 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAhCVGPDVKDLAALR	lekrIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAhCVGPDVKDLAALR	62 VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASET	62 VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGAJIALLELEEPVNVSSHVHTVTLPPASET	62 VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASET	62 VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASET	62 VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASET
.8	- E	60	- 8	>	ı,	-8	,	- -	- 8	18	9 - 8	-8		8-	
- 59	-09-598	-09-598	-09-598	865-60	09-598	-09-598	-09-598	-09-598	-09-598	consensus	365-60-SD	365-60	09-598	965-60	-865-60
00-SU	-SD	US-	us-	US-	0-SU	US-	TUS-	US-	ns-	Ö	-SN	ns-	us-	ns-	0-SU

2 VQLKEQHLYYQDQLLEVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASET	VOLRECHLYYODOLLPVSRIIVHPOFYTAQIGAAIALLELE	VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELR	 DIALLELE	VQLREQHLYYQDQLLEVSRIIVHPQFYTAQIGAdIALLELBEPVKVSSHVHTVTLPPASET	PPGMPCWVTGWGDVDNDRRLPPFPLKOVKVPIMENHICDAKYHLGAYTGDDVR	PPGMPCWVIGWGDVDNDERLPPPFLKQVKVPIMBNHICDAKYHLGAYTGDDVR.	PPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVR.	FPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVR	PPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDM	FPEGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVR:	FPEGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVR	FPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAXYHLGAYTGDDVR	FPPGMPCWVIGWGDVDNDERLPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVR.	FPPGMPCWVTGWGDVDNDERLEPPFFLKQVKVPIMENHICDAKYHLGAYTGDDVR1	FPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDM	LCAGNTRRDSCQGDAGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTREDSCQGDAGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTREDSCQCDAGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTRRDSCQGDAGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG1YTRVTYYLDWIHHY	184 LCAGNTRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY	LCAGNTREDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG1YTRVTYYLDWIHHY	LCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG1YTRVTYYLDWIHHY	LCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGBGCAQPNRPGIYTRVTYYLDWIHHY	;>-	-;>-		->-			VPKKP 
62	62	62	28		123	123	123	123	/123	123	123	123	123	119		184	184	184	184	184	184	184	184	184	180		245	245	245	245	245	245	245
US-09-598- US-09-598-	-865-60-SD	US-09-598-	US-09-598-	consensus	US-09-598-	US-09-598-	US-09-598-	US-09-598-	9-59	US-09-598-	US-09-598-	1	US-09-598-	US-09-598-	consensus	-869-60-SD	-865-60-SD	US-09-598-	US-09-598-	~-865-60-SU	US-09-598-	US-09-598-	US-09-598-	US-09-598-	US-09-598-	consensus	US-09-598-	US-09-598-	US-09-598-	Ň		US-09-598-	US-09-598-

US-09-598- 241 VPKKP US-09-598- 245 VPKKP US-09-598- 245 VPKKP

consensus

VPKKP

Alignment score = 2213.00

Scoring matrix:

16	247	223	246	246	248	248	247	247	249	
15	247	223	246	246	248	248	247	247		
14	247	223	246	248	246	246	247			
13	247	223	248	246	246	246				
8	248	224	247	247	249					
7	248	224	247	247						
9	248	224	247							
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4	225									
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GENALIGN - Multiple Sequence Alignment Program Release 5.4

Fri 23 Jul 104 8:12:22-PDT

Solution Parameters:

Nucleic Alphabet = Identity
Coutput line length = 80
Compress = Off
Histogram = Off
Randomization = Off

AMINO-Res-length = 0ff
AMINO-Res-length = 2
DELetion-weight = 5.00
LEngth-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
SPread-factor = 50

Clustered order of selected sequences:

뉴	-	- 1	4	4	4	(1-771)	- 1	- 1	•	
US-09-598-982-4	US-09-598-982-2	US-09-598-982-	US-09-598-982-4	US-09-598-982-3	US-09-598-982-2	6. US-09-598-982-8	US-09-598-982-2	US-09-598-982-	US-09-598-982-1	
,	13	37	56	2	1,	v	16	24	1-	

Region Alignment: (listed in Clustered order)

US-09~598-	-	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGC
US-09-598-	1	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCAAGGAGCAAGTGGCCCTGGG
US-09-598-	7	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCCTGGC
US-09-598-	Н	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGCCTGGCCTGGG
US-09-598-	н	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAAGGAGAAAGGAGCCCCTGG
US-09-598-	Н	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAAGGAGGAAAGGGCCCTGGC
US-09-598-	Н	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAAGGAGAAAGGGCCTGGC
US-09-598-	1	GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAAGGAGCAAGTGGCCCTGGG
US-09-598-	7	GGGCCCCTCGAGAAAGAATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGCCCTGG
US-09-598-	7	ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGC
consensus		999cccctcgagaaaagaATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGC
US-09-598-	62	AGGIGAGCCIGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCA
US-09-598-	62	AGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTCCGGGGGGCTCCCTCATCCA
US-09-598-	62	AGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTCCGGGGGGCCTCCCTC
US-09-598-	62	AGGTGAGCCTGAGGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCA
-865-60-SD	62	AGGTGAGCCTGAGAGTCCACGGCCCATACTGGACTTCTGCGGGGGGCTCCCTCATCCA

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This Paga Biank (Uspia)

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## GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

0.001 Seconds ; Search time July 23, 2004, 08:23:52 Run on:

OM protein - nucleic search, using frame\_plus\_p2n model

(without alignments) 383.958 Million cell updates/sec

US-09-598-982-9 Title: Perfect

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1 segs, 771 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

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GENERAL INFORMATION:
APPLICANT: MAFFITY MARK
TITLE OF INVENTION: THECOMBINANT PROTECUTIC TYPTASES, ACTIVE SITE MUTANTS
TITLE OF INVENTION: THEORY, AND METHODS OF MAKING SAME
TITLE OF INVENTION: THEORY, AND METHODS OF MAKING SAME
TITLE OF ILLING DATE: 2000-06-21
CURRENT APPLICATION NUMBER: US/09/599,982
CURRENT APPLICATION NUMBER: 09/079,970
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ IED NOS: 51
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ORGANISM: Homo sapiens
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Search completed: July 23, 2004, 08:23:53 Job time: 0.001 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run

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Pentunga Fatents NA Main: US-09-599-982-10

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10:
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-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                            (without alignments)
0.360 Million cell updates/sec
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nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NILES, ANDREW L
APPLICANT: NILES, ANDREW L
APPLICANT: HAAK FRENDSCHO, MARY
APPLICANT: HAAK FRENDSCHO, MARY
TITLE OF INVENTION: RECOMBINANT PROTECLYTIC TYPTASES, ACTIVE SITE MUTANTS
TITLE OF INVENTION: THEREOF, MAN METHODS OF MAKING SAME
FILE REPRENCE: CIP TRYPTASE
CURRENT APPLICATION NUMBER: US/09/598,982
CURRENT FILING DATE: 1090-06-15
PRIOR APPLICATION NUMBER: 09/079,970
PRIOR APPLICATION NUMBER: 09/079,970
SROFTWARE: PATENTING DATE: 1098-04-15
SOFTWARE: PATENTING PATE: 100-06-15
SOFTWARE: PATENTING PATE: 100-06-15
SOFTWARE: PATENTING PATE: 100-06-15
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ORGANISM: Homo sapiens
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180 200 120 140 CCGGGGATGCCCTGCTGGTCACTGGCTGGGCGATGTGGACAATGATGAGGCCCTCCCA 420 160 480 540 009 220 240 GTGAAGGTCTCCAGCCACGTCCACGTCACCCTGCCCCCTCGCTCAGAGACCTTCCCC 360 720 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 161 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu VallysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro ProProPheProLeuLysGlnValLysValProlleMetGluAsnHisIleCysAspAla CCGCCATTCCTCTGAAGCAGGGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA AAATACCACCTTGGCGCCTACACGGGGGGGCGTCCGCTCGTCGTCGTGACGACGACGTG CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 541 TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTC LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 241 ValProLysLysPro 245 GICCCCAAAAAGCCG 735 81 101 301 121 361 141 421 481 181 201 g ò g g ð g g q 8 B 8 g ò δ ò

Search completed: July 23, 2004, 08:25:04 Job time : 1 secs

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Compugen Ltd.
GenCore version (c) 1993 - 2004
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Run

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29: /cgm2_6/ptodata/2/pna/US08_COMB.seq:US-09-598-982-20
29: /cgm2_6/pt
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-DB=Pending Patents NA Main:US-09-598-982-20 -SUFFIX=pto -OUT-align21_20
-MINMATCH=0.1 -LOOPGIN=0 -LOOPEXT=0 -UNITS=bits -START=1 -BND=-1
-MATRIX-Blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MDDB=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
                                                             search time 1 Seconds
(without alignments)
0.384 Million cell updates/sec
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1 LEKRIVGGQEAPRSKWPWQV....IYTRVTYXLDWIHHYVPKKP
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGGGGGGCTCCCTCATCCACCCC 126
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APPLICANT: MARK A
APPLICANT: MARK A
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: RECOMBINANT PROTECLYTIC TYPTASES, ACTIVE SITE MUTANTS
TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
FILE REFERENCE: CIP TRYPTASE
CURRENT APPLICATION NUMBER: US/09/598,982
PRIOR PILING DATE: 09/079,970
PRIOR PILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Datentin Ver. 2.0
SEQ ID NO 20
LENGTH: 771
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Sequence 22, Application US/0959892

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Sequence 22, Application:

APPLICANT: NILES, ANDREW L

APPLICANT: MARK A

APPLICANT: HAAK-REENDSCHO, MARY

TITLE OF INVENTION: THERROF, AND METHODS OF MAKING SAME

TITLE OF INVENTION: THERROF, AND METHODS OF MAKING SAME

TITLE OF INVENTION: THERROF, AND METHODS OF MAKING SAME

TITLE OF INVENTION: US 09/9598,982

CURRENT FILING DATE: 2000-06-21

PRIOR PILITING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 771

TYPE: DNA

CORGANISM: Homo sapiens
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                                          GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC
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## Compugen Ltd. 5.1.6 GenCore version Copyright (c) 1993 - 2004

OM protein - nucleic search, using frame\_plus\_p2n model

Seconds ; Search time 0.001 July 23, 2004, 08:29:03 on:

(without alignments)
383.958 Million cell updates/sec

LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP US-09-598-982-25 1397 Title: Perfect score: Sequence:

249

**BLOSUM62** Scoring table:

0 0 2 2 00.4 , Xgapext , Ygapext , Fgapext , Delext Xgapop 10.0 Ygapop 10.0 Fgapop 6.0 Delop 6.0

residues 771 seds,

N Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

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rending Patents NA Main: US-09-598-982-24

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10. /cg Pending Database

align25 24

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/cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-24
                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGTGGGTGCTGACCGCACGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC
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US-09-588-982-24

Sequence 24, Application US/09598982

Sequence 24, Application US/09598982

GENERAL INFORMATION

APPLICANT: NILES, ANDEW L

APPLICANT: HAAK FRENDSCHAC, MARY

TITLE OF INVENTION: THEREOF, AND METHODS OF MAK.

FILE REPERENCE: CIP TRYPTASE

CURRENT APPLICATION NUMBER: US/09/598,982

CURRENT FILING DATE: 2000-06-21

PRIOR APPLICATION NUMBER: 09/079,970

PRIOR PILING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-598-982-25 (1-249) x US-09-598-982-24 (1-771)
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LENGTH: 771
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                                247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCTGCTGGAG
                                                                   GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis
                                                                                                              427 GAGCGCCCCCCCACCGCCATTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC
                                                                                                                                     IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArg
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                                                                                                                                                                       AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly
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nucleic search, using frame\_plus\_p2n model

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protein

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(without alignments) 0.384 Million cell updates/sec July 23, 2004, 08:29:57; Search time 1 Seconds Run on:

LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP US-09-598-982-27 1397 Title: Perfect score: Sequence:

249

0022 , Xgapext , Ygapext , Fgapext , Delext Xgapop 10.0 Ygapop 10.0 Fgapop 6.0 Delop 6.0 **BLOSUM62** Scoring table:

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seq length: 0 seq length: 200000000 Minimum DB Maximum DB Minimum Match 0% Maximum Match 100% Listing first 1 summaries Post-processing:

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246
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APPLICANT: MILES, ANDREW L
APPLICANT: MARK A
APPLICANT: MARK-FRENDSCHO, MARY
TITLE OF INVENTION: RECOMBINANT PROTECLYTIC TYPTASES, ACTIVE SITE MUTANTS
TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
TITLE REFERENCE: CID TRYPHASE
CURRENT APPLICATION NUMBER: US/09/598,982
PRIOR PILING DATE: 09/079,970
PRIOR PILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Datentin Ver. 2.0
LENGTH: 771
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US-09-598-982-26
Sequence 26, Application US/09598982
GENERAL INFORMATION:
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US-09-598-982-37 1394 Title: Perfect score:

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0022 , Xgapext , Ygapext , Fgapext Delext . . . BLOSUM62 Xgapop 10.0 , Ygapop 10.0 , Fgapop 6.0 , Delop 6.0 ,

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

parameters:

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RESULT 1
US-09-598-982-36
Sequence 36, Application US/09598982
GENERAL INFORMATION:
APPLICANT: MAFFITT, MARK A
APPLICANT: HAAK RENDSCHO, MARY
TITLE OF INVENITON: THEREOF, AND METHODS OF MAKING SAME
TITLE OF INVENITON: THEREOF, AND METHODS OF MAKING SAME
TITLE OF INVENITON: THEREOF, AND METHODS OF MAKING SAME
TITLE OF INVENITON: THEREOF, AND METHODS OF MAKING SAME
CURRENT APPLICATION NUMBER: 09/079,982
CURRENT FILING DATE: 2000-06-21
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
TENGTH: 771
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Search completed: July 23, 2004, 08:34:10 Job time: 1 secs

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(without alignments) 383.958 Million cell updates/sec

US-09-598-982-39

Title: Perfect score:

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APPLICANT: NILES, ANDREW L
APPLICANT: NILES, ANDREW L
APPLICANT: MAFFITT, MARK A
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: RECOMBINANT PROTECLYTIC TYPTASES, ACTIVE SITE MUTANTS
TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
FILE REFERENCE: CIP TRYPTASE
CURRENT APPLICATION NUMBER: US/09/598,982
CURRENT FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 09/079,970
PRIOR FILING DATE: 1998-04-15
SOFTWARE: PATENTING DATE: 2.0
SOFTWARE: PATENTING DATE: 1998-04-15
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completed: July 23, 2004, 08:35:03 le: 0.001 secs time Search Job tim

5.1.6 Compugen Ltd. version -GenCore

Seconds July 23, 2004, 08:35:57 ; Search time 0.001 on:

nucleic search, using frame\_plus\_p2n model

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(without alignments)
383.958 Million cell updates/sec

US-09-598-982-41 1398 Title: Perfect score:

LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP Scoring table: Sequence:

, Xgapext , Ygapext , Fgapext , Delext BLOSUM62 Xgapop 10.0 , Ygapop 10.0 , Fgapop 6.0 , Delop 6.0 ,

residues 771 1 segs, Searched:

hits satisfying chosen parameters: Total number of

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

Command line parameters:

Pending Database

-DELOP=6 -DELEXT=7

-YGAPEXT=0.5

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US-09-588-982-40

Sequence 40, Application US/09598982

Sequence 40, Application US/09598982

Sequence 40, Application US/09598982

Sequence 40, Application US/09598982

APPLICANT: MILES, ANDREW L

APPLICANT: MARK A

TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME

FILE REFERENCE: CIP TRYPTICS,

CURRENT APPLICATION NUMBER: US/09/598,982

CURRENT APPLICATION NUMBER: 09/079,970

PRIOR APPLICATION NUMBER: 09/079,970

PRIOR PILING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGTCCCTCATCCACCCC 126
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Compugen Ltd
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version -
 GenCore
Copyright (c) 1993
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Seconds July 23, 2004, 08:36:46 ; Search time 0.001 Run on:

nucleic search, using frame\_plus\_p2n model

protein

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(without alignments)
383.958 Million cell updates/sec

US-09-598-982-43 1398 Title: Perfect score:

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249

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residues 1 seds, 771 Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

Command line parameters:

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12. /cgn2\_6/ptodata/2/pna/USO8\_COMB.seq.US\_09-598-982-42

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align43

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RESULT 1
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; APPLICANT: MARK A
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
; TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
; CURRENT PILING DATE: 000-06-21
; PRIOR PAPLICATION NUMBER: 09/079,970
; PRIOR APPLICATION NUMBER: 09/079,970
; PRIOR PILING DATE: 1998-04-15
; OUTHWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                        Sequence 42, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AGCCTGAGAGTCCAGGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC 126
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/cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-42
/cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-42
/cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-42
/cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-42
/cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-42
/cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-42
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                                                                                    GAGCGCCTCCCACCGCCATTCCTCTGAAGCTGAAGGTCCCCCATAATGGAAAACCAC
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                                          LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2004, 13:26:16; Search time 52 Seconds (without alignments) 249.336 Million cell updates/sec Run on:

US-09-598-982-21 1393 1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP 249 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues

Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		P20231 homo sapien	homo	homo	P21845 mus musculu	4	-	-	P50343 rattus norv	rattus	Q9xsm2 ovis aries	Q9n2dl sus scrofa	O9bzj3 homo sapien	canis			homo	rattu	Q9esd1 mus musculu	Q16651 homo sapien	homo	homod	mus m	mus	Q9jhj7 mus musculu	homo	homod	Q9dbi0 mus musculu	mus	5 homo	0 homo	3 homo	52 homo	10 equue
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	KAL MOUSE	PLMN BOVIN	KAL RAT	EL2_RAT	PLMN CANFA	CTRB_BOVIN	PLMN_SHEEP	EL2A HUMAN	TMS2_MOUSE	EL2 MOUSE	TMS4 MOUSE	PLMN_HUMAN	
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99432168; PubMed=10500112; Stubbs M.T., Spamerhoff C.P., Bode W., Pereira P.J.B., Matschiner G., Bergner A.; Stuerzebecher J., Pricchottka G.P., Matschiner G., Bergner A.; The structure of the human betall-tryptase tetramer: fo(u)r better or
                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE=99180625; PubMed=9521329;
Pereira P.J.B., Bergmer A., Macedo-Ribeiro S., Huber R.,
Matschiner G., Fritz H., Sommerhoff C.P., Bode W.;
"Human beta-tryptase is a ring-like tetramer with active sites facing
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatatne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Stangola A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Schmutz J., Myers R.M., Schein J.E., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 96:10984-10991(1999).
-!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
-!- CATALITIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mast cell activation.
POLYMORPHISM: There are two alleles; beta-II and beta-III which differ by 3 residues.
SIMILARITY: Belongs to peptidase family SI. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Released from the secretory granules upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:14120; TPSB2.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
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InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
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EMBL, M33492, AAA3679.1; -.
EMBL, M33493, AAA36780.1; -.
EMBL, S55551, AAD13876.1; -.
EMBL, AF099143; AAD17859.2; -.
EMBL, AF099144; AAD17888.1; -.
EMBL, BC029356; AAH29356.1; -.
                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences.
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PRINTS; PR00722; CHYMOTRYPSIN.
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PDB; 1AAO; 31.JAN-94.
PDB; 1AOL; 23.JAR-99.
MEROPS; S01.027; --
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211 CAGNIRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIXTRVTXYLDWIHHY 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90251647; PubMed-2187193;
Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q15661; Q15663; Q9H2A;
16-OCT-2001 (Rel. 49, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tryptase beta-1 precursor (EC 3.4.21.59) (Tryptase)
TPSB1.
                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                               98.2%; Score 1368; DB 1; Length 275; 99.6%; Pred. No. 2.6e-118; ive 0; Mismatches 1; Indels (
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (PC

HGP -> RDR (IN BETA-III) .

/FTIG-VAR 012104 .

K -> N (IN REF. 3) .

ZB27396CS1F5C7A0 CRC64;
                                                                                                 POTENTIAL.
ACTIVATION PEPTIDE.
TRYPTASE BETA-2.
CHARGE RELAX SYSTEM.
CHARGE RELAX SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine protease family.";
Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
                                                                                                                                                                                                                                                                                                                                                                                               30529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 99.6%;
Les 244; Conservative
                                                                                    Polymorphism; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                 275 AA;
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SEQUENCE FROM N.A.
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                                                                  "Molecular cloning and characterization of novel human tryptase cDNAs
                                                                        IsoId=Q15661-2; Sequence=VSP_005375;
SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (in isoform 2).
F-Id=VSP_005375.
A -> V (in dbSNP:1800984).
F-Id=VAR_014557.
G -> V (in dbSNP:1800986).
                   SEQUENCE OF 54-275 FROM N.A. (ISOFORM 2).
Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATION PEPTIDE (BY SIMILARITY) TRYPTASE BETA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R InterPro; IPR009003; Cys Ser trypsin.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001214; Peptidase_S1.
R InterPro; IPR001314; Peptidase_S1.
R Pfam; PF00089; trypsin; 1.
R PROSITE; PS50240; TRYPSIN DOW; 1.
R PROSITE; PS50240; TRYPSIN DOW; 1.
R PROSITE; PS00134; TRYPSIN ESS; 1.
R Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen; Alternative splicing; Polymorphism.
SIGNAL 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VAR 014558.
A -> T (in dbSNP:2234902).
/FTId=VAR 014559.
N -> K (in dbSNP:1800991).
                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                 IsoId=Q15661-1; Sequence=Displayed;
Biol. Chem. 274:3355-3362(1999)
                                                                                                                                                                                                                                                                                                                                                                                EMBL; M33494; AAC83172.1; -.
EMBL; M33491; AAA36778.1; -.
EMBL; AF099144; AAD17866.1; -.
BMBL; AF206667; AAG35697.1; -.
PIR; A35863; A35883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.242; -
Genew; HGNC:12019; TPSB1.
                                                                                                                                                                                    mast cell activation. ALTERNATIVE PRODUCTS:
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                                                        Hunt J.E.;
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211 CAGNTREDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFP 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 PGMPCWVTGWGDVDNDERLPPPFFLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 CAGNTRRDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
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MEDLINE=99121069; PubMed=9920877;
Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
"Characterization of genes encoding known and novel human mast cell
tryptases on chromosome 16p13.3.";
J. Biol. Chem. 274:3355-3362(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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                                                                                                               /FTIG-VAR 014561.

P -> S (in dbSNP 2234904).

/FTIG-VAR 01452.

T -> S (in dbSNP 2234905).

/FTIG-VAR 014563.

R -> Q (in dbSNP 2234906).

/FTIG-VAR 014563.
/FTId=VAR_016102.
T -> A (in dbSNP:1800992).
/FTId=VAR_014560.
D -> N (in dbSNP:2234641).
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                                                                                                                                                                                                                                                                                                  FTId=VAR 014564.
ADC48FDC51F37112 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P15157; Q9H2Y5; Q9UQI1;
01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-tryptase precursor (EC 3.4.21.59) (Tryptase 1).
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J. Clin. Invest. 84:1188-1195(1989)
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MEDLINE=90009311; PubMed=2677049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                 275 AA; 30515 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.2
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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SEQUENCE OF 32-54
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                                                                                                                                                                    MEDLINE=87109258; PubMed=3543004;
Cromlish J.A., Seidah N.G., Marcinkiewcz M., Hamelin J., Johnson D.A.,
                                                        "Molecular cloning and characterization of novel human tryptase cDNAs
                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Released from the secretory granules upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P15157-2; Sequence=VSP_005374;
SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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SIMILARITY).
SIMILARITY).
Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J., Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R MIM; 191080; -.

R GO; GO:0008236; F:serine-type peptidase activity; TAS.
GO; GO:0008235; P:defense response; TAS.
R GO; GO:0006925; P:defense response; TAS.
R InterPro; IPR00303; Cys Ser trypsin.
R InterPro; IPR001254; Peptidase_S1A.
R Pfau, PF00089; trypsin; 1.
R Pf00089; trypsin; 1.
R PROSITE; PS50240; TRYPSIN DOM; 1.
R PROSITE; PS50240; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN BIS; 1.
R PROSITE; PS00135; TRYPSIN BIS; 1.
R PROSITE; PS00135; TRYPSIN SER; 1.
R PAGACLASE; Serine procease; Signal; Glycoprotein; Zymogen; PP1/morphism; Alternative splicing.
                                                                                             Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                 [5]
SEQUENCE OF 31-50, AND PITUITARY, SEQUENCE OF 31-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
ACTIVATION PEPTIDE.
ALPHA-TRYPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P15157-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M30038; AAA86934.1; -.
EMBL; AF088328; AAD17846.1; -.
EMBL; AF206665; AAG35695.1; -.
EMBL; AF2066666; AAG35696.1; -.
HSSP; P20231; IAOL.
                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P20231; 1A0L.
MRROPS; S01.015; -.
MRROPS; S01.143; -.
Genew; HGNC:12018; TPS1.
MIM; 191080; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   mast cell activation. ALTERNATIVE PRODUCTS:
                                                                            variants.";
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                                                                                                                                                                                                                                                                                                                                                                                 31 IVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHCLGPDVKDLATLRVQL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94023807; PubMed=8210998;
Huang R., Abrink M., Gobl A.E., Nilsson G., Aveskogh M., Larsson L.G.,
Nilsson K., Hellman L.;
"Expression of a mast cell tryptase in the human monocytic cell lines
U-937 and Mono Mac 6.";
Scand. J. Immunol. 38:359-367(1993).
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MEDLINE=95048582; PubMed=7959952;
Huang K., Hellman L.T.;
"Genes for mast-cell serine protease and their molecular evolution.";
Immunogenetics 40:397-414(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 PGMPCWVTGWGDVDNDEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
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                  /FTId=VSP_005374.

R -> P (IN ALPHA-II).

/FTId=VAR_012102.

K -> Q (IN ALPHA-II; dbSNP:1137382).

/FTId=VAR_012103.

/FTIG=VSR_012103.

TR -> SQ (IN REF. 1).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Reynolds D.S., Gurley D.S., Austen K.F., Serafin W.E.;
"Cloning of the cDNA and gene of mouse mast cell protease-6.
Transcription by progenitor mast cells and mast cells of the connective tissue subclass.";
J. Biol. Chem. 266:3847-3853(1991).
                                                                                                                                                                                                                                                                                   13; Indels
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P21845; Q61962;
01-MM2-1991 (Rel. 18, Created)
10-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mast cell protease 6 precursor (EC 3.4.21.59)
                                                                                                                                                                                                                             92.0%; Score 1282; DB
93.1%; Pred. No. 2e-11
live 4; Mismatches
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30772 MW;
                                                                                                                                                                                                                                                        Local Similarity 93.1
nes 228; Conservative
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275 AA;
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GUGGBU OGLONAC. . .) (POTENTIAL).

FINED ONS 376.
                            Serafin W.E.,
"Different mouse mast cell populations express various combinations of at least six distinct mast cell serine proteases.",
Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990)
-I- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
                                                                                                                                                                                                                                                                    Note=Probably non functional; SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                         CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%; Score 1091; DB 1; Length 276; 78.2%; Pred. No. 7e-93; tive 19; Mismatches 34; Indels (
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART: SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
HYDROLAGE; Serine protease; Signal; Glycoprotein; Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform Short). /FIId=VSP 005377.
                                                                                                                                                                                                                                      Name=Short;
IsoId=P21845-2; Sequence=VSP_005376, VSP_005377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 AA; 30927 MW; 525B2C9A04A72200 CRC64;
                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:96942; Mcpt6.
GO; GO:0008201; F:heparin binding; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0030019; F:tryptase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR009003, Cys Ser trypsin.
InterPro, IPR001254; Peptidase S1.
InterPro, IPR001314; Peptidase_S1A.
MEDLINE=90222202; PubMed=2326280;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, MS7626; AAA39988.1; --
EMBL, MS7625; AAA39987.1; --
EMBL, L31853; AAA39125.1; --
EMBL, X78542; CAA55288.1; --
PIR; A38654; A38654.
PIR, A48685; 148685.
HSSP, P20231; 1AAO.
                                                                                                                                                                         ALTERNATIVE PRODUCTS
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                                                                                                                                        125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
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                                                                                                     REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFF 124
MEDIINE-89352460; PubMed-2504277;
Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
"Molecular cloning of dog mast cell tryptase and a related protease:
structural evidence of a unique mode of serine protease activation.";
Biochemistry 28:4148-4155(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
-!- CATALITIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
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-:- SUBCELLULAR LOCATION: Released from the secretory granules upon mast cell activation.
-:- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 canis ramiliaris (1009).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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ACTIVATION PEPTIDE (BY SIMILARITY).
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tryptase precursor (EC 3.4.21.59).
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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HSSP; P20231; 1AAO.
MEROPS; S01.143; -.
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P15944;
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MGS/SEA, TISSUE=Intestine, MEDLINE=95366971; PubMed=763971; Murakumo Y., 1de H., Itoh H., Tomita M., Kobayashi T., Murakumo Y., 1de H., Yowa Y.; "Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones unguiculatus, and its preferential expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 309:921-926(1995).
-!-CATALTYIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
-!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mast cell tryptase precursor (EC 3.4.21.59).
Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
          CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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N'LINKED (GLCMAC. . .) (POTENTIAL).
W, C3B869251P248D5B CRC64;
            SIMILARITY).
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                                                                                                                                          77.3%; Score 1077; DB 1; Length 275; 77.1%; Pred. No. 1.3e-91;
                                                                                                                                                                    35; Indels
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                                                                                                                                                                    21; Mismatches
                                                                                                                   30088 MW;
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                                                                                                                                                       77.18;
                                                                                                                                                                    Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
275
74
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                                                                                                     132
275 AA;
                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             271 VPKEP 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 PGMPCWVTGWGDVDNDERLPPPFFLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.2%; Score 1075; DB 1; Length 270; 77.4%; Pred. No. 2e-91;
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(BY
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          InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
PR0018089; trypsin; 1.
PR00182; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PR0SITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00113; TRYPSIN JEX; 1.
PROSITE; PS00113; TRYPSIN SER; 1.
Hydrolase; Serine protease; Signal; Glycoprotein.
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01-JUL-1993 (Rel. 26, Last sequence update)
01-BFEB-2003 (Rel. 41, Last annotation update)
Mast cell protease 7 precursor (EC 3.4.21.59)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC
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270
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116
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270 AA;
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MEROPS; S01.143;
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Fri Jul

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                                                                                                                                                                                                                                            Comment=The alternative splicing event is due to a G to A point mutation at the exon 2/intron 2 splice site and causes loss of protein expression. The alternatively spliced transcript is only
                                                                                                                                                                                                                                                                                                                                     Name=2; Synonyms=Truncated;
IsoId=Q02844-2; Sequence=VSP 005378, VSP 005379;
DEVELOPMENTAL STAGE: Is not expressed in mature serosal or mucosal
mast cells and is expressed only transiently at an early stage of
in vitro mast cell differentiation.
                                                                                                                   J. Biol. Chem. 271:2851-2855 (1996).
-!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
-!- CATALYIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMRAT; SM00200; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Signal; Zymogen; Alternative splicing;
                                                                         Ghildyal N.; "Natural disruption of the mouse mast cell protease 7 gene in the C57BL/6 mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                           MEDLINE=96162035; PubMed=8576265;
Hunt J.E., Stevens R.L., Austen K.F., Zhang J., Xia Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50ECB4765294205E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAST CELL PROTEASE 7.
                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L00654; AAA39993.1; --
EMBL; L00653; AAA39993.1; --
EMBL; U42405; AAA3982.1; --
EMBL; U42406; AAA37874.1; --
EMBL; U42466; AAA37875.1; --
PIR; A47246; AA7246.
MEXOPS; S01.026; --
MGD; MGI:95943; MCpt7.
InterPro; IPR003003; Cys_Ser_trypsin.
InterPro; IPR001314; Peptidase S1.
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[2]
SEQUENCE FROM N.A. (ISOFORM 2)
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                                                                                                                                                                                                                                                                                            found in C57BL/6 mouse;
                                                                                                                                                                                                                 -!- ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
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SIGNAL
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                                                                                                                                                              65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEFVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                             125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                   64
                                                                                                                                                                                    209 CAGNEGHDSCQCDSGGPLVCKVEDTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
                                                                                                                29 IVGGGEAHGNKWPWQVSLRANDTYWMHFCGGSLIHPQWVLTAAHCVGPDVADPNKVRVQL
                                                                                                                                                                                                                                                                    149 SGTLCWVTGWGNIDNGVNLPPPFPLKEVQVPIIENHLCDLKYHKGLITGDNVHIVRDDML
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                                         Gaps
                                                                                 5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague Dawley, TISSUE-Peritoneal mast cells;
MEDLINE=97149430; PubMed=8996238,
Lutzelschwab C., Pejler G., Aveskogh M., Hellman L.;
Secretory granule proteases in rat mast cells. Cloning of 10
different serine proteases and a carboxypeptidase A from various rat
mast cell populations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Exp. Med. 185:13-29(1997).
-!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
-!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P50343; P97593;
01-0CT-1996 (Rel. 34, Last equence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mast cell protease 6 precursor (BC 3.4.21.59) (RMCP-6) (Tryptase).
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Ide H., Itoh H., Tomita M., Murakumo Y., Kobayashi T.,
Maruyama H., Osada Y., Nawa Y.;
Maruyama H., Osada Y., Nawa Y.;
"CDNA sequencing and expression of rat mast cell tryptase.";
J. Biochem. 118:1210-215(1995).
Length 273;
                                         Indels
                                           40;
75.7%; Score 1054; DB 1; 76.5%; Pred. No. 1.7e-89;
                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Peritoneal mast cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D38455; BAA07486.1; -. EMBL; U67909; AAB48262.1; -.
                                     Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
  Query Match
Best Local Similarity
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Score 1037;
                           Exp. Med. 185:13-29(1997)
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                                                                                                                                                                                                                                       -!- SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                          mast cell activation.
                                                                                                                                                                                                                                                                                                                                                                                     PIR; A23698; A23698.
PIR; S21275; S21275.
HSSP; P20231 IAAO.
MEROPS; S01.026; -.
MEROPS; S01.143; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 AA;
                                                                                                               SEQUENCE OF 29-51.
                                               SEQUENCE OF 29-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Serine
Multigene family.
SIGNAL
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                              90 REQYLXYADQLITVNRTVVHPHYYTVEDGADIALLELEIPVNVSTHIHPISLPPASETFP 149
                                                                                                                                                                                                                                                                                                                                                                                                  SGTSCWVTGWGDIDSDEPLLPPYPLKQVKVPIVENSLCDRKYHTGLYTGDDVPIVQDGML 209
                                                                                                                                                                                                                                                                                                                                                                                                                                         210 CAGNTRSDSCQGDSGGPLVCKVKGTWLQAGVVSWGEGCAEANRPGIYTRVTYYLDWIHRY 269
                                                                                                                                                                                                                                                                                                                                                    REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                        125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                          5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                              CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                        EX SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P27435; P27436;
01-AUG-1992 (Rel. 23, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mast, cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Tryptase,
                                                                                                                                                   SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                          75.4%; Score 1051; DB 1; Length 274; 75.8%; Pred. No. 3.3e-89;
                                                             PRINTS, PRO0722, CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOW, 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN ERR; 1.
Hydrolase; Serine protease; Glycoprotein; Multigene family;
                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                   I -> N (IN REF. 2).
I -> T (IN REF. 2).
DF84D55668CA1A25 CRC64;
                                                                                                                               ACTIVATION PEPTIDE.
MAST CELL PROTBASE 6.
CHARGE RELAY SYSTEM (BY S.
CHARGE RELAY SYSTEM (BY S.
CHARGE RELAY SYSTEM (BY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;
MEDLINE=97149430; PubMed=8996238;
Lutzelschwab C., Pejler G., Aveskogh M., Hellman L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 AA
                                                                                                                                                                                                                                                                                             21; Mismatches
        MSSP, P20231; 1AAO.
MEROPS; S01.025; -
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR011254; Peptidase_S1.
InterPro; IPR011314; Peptidase_S1.
PF00089; trypsin; 1.
                                                                                                                                                                                                                                                        30508 MW;
                                                                                                                                                                                                                                                                                            Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                        19
29
274
73
120
223
74
PIR; JC4171; JC4171.
                                                                                                                                                                                                                                                       274 AA;
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPKK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPQR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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20
30
73
73
73
120
120
104
104
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                                                                                                                                        CHAIN
ACT SITE
ACT SITE
ACT SITE
DISULFID
                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                              Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                             a novel
"Secretory granule proteases in rat mast cells. Cloning of 10 different serine proteases and a carboxypeptidase A from various rat mast cell populations.";
                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Mast cells.
-!- PTM: Glycosylated (Probable).
-!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
SIMILARITY)
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(IN REF. 3).
WLP (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Zymogen; Signal;
                                                                                                                                               STRAIN=Sprague-Dawley, TISSUE-Skin,
MEDLINE=91242400; PubMed=2036367;
Braganza V.J., Simmons W.H.;
"Tryptase from rat skin: purification and properties.";
Biochemistry 30:4997-5007(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POIDER ACTIVATION PEPTILL.
ACTIVATION PEPTILL.
CHARGE RELAY SYSTEM (BY SII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65A5ED4D279FB284 CRC64;
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CHARGE RELAY SYSTEM (
BY SIMILARITY.
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BY SIMILARITY.
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF001089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PSS0240; TRYPSIN_DM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
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                                                                                                                                    REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                         125 PGMPCWVTGWGDVDNDERLPPPFFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                  CAGNEGHDSCQGDSGGPLVCKVEDTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIYRY 268
                                                                                                                                                                                                                                                                                     CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                        IVGGQEASGNKWPWQVSLRVNDTYWMHFCGGSLIHPQWVLTAAHCVGFNKADPNKLRVQL
                                                         IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pemberton A.D., McAleese S.M., Huntley J.F., Collie D.D.S., Scudamore C.L., McBuen A.R., Walls A.F., Miller H.R.P.; "CDNA sequence of two sheep mast cell tryptases and the differential expression of tryptase and sheep mast cell proteinase-1 in lung, dermis and gastrointestinal tract."; Clin. Exp. Allergy 30:818-832(2000).
-!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with more restricted specificity than trypsin.
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Released from the secretory granules upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; NCBI TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                     37; Indels
   Pred. No. 6.3e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB 2 precursor (EC 3.4.21.59).
Ovis aries (Sheep).
                     21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Abomasum;
MEDLINE=20308142; PubMed=10848900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y18224; CAB41989.1; -. HSSP; P20231; 1AAO.
   76.18;
                     Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mast cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              VPK 247
                                                                                                                                                                                                                                                                                                                                                                                                269 VPK 271
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PRINTS; PR00722; CHYMOTRYPSIN

Pfam, PF00089; trypsin,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSQCWVTGWGDVDNGRPLPPPYPLKQVKVPIVENSVCDWKYYSGLSTDXSVPIVQEDNL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 IIGGKEAPGSRWPWQVSLRVRDQYWRQCGGSLIHPQWVLTAAHCIGPELQEFSDFRVQL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M., Yano M., Yang B., Kido H.; Towatari T., Tashiro J., Murakami M., Yano M., Yang B., Kido H.; Tunga triggers infection by pneumotropic Sendai and infiluenza A viruses. Purification and characterization."; Eur. J. Biochem. 267:3189-3197(2000).

-!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGFDVKDLAALRVQL
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELULAR LOCATION: Released from the secretory granules upon mast cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metāzoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                          ACTIVATION PEPTIDE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.9%; Score 1030; DB 1; Length 273; 73.1%; Pred. No. 2.8e-87;
                                                                                                                    Glycoprotein; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MCT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Mismatches
                                                                                                                                                                                                     TRYPTASE 2.
                                                                                                                                            POTENTIAL
                                                                                                              Hydrolase; Serine protease; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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SMART; SM00020; Tryp_SPc; 1.
SMSGITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30288 MW;
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273
72
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222
57
153
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ACT SITE
ACT SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Best Local
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                                                                                                                                         SIGNAL
                                                                                                                                                                       PROPEP
  SPITITION SOLUTION SELECTION SPITITION SPITITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 GEQHLYYQDRLLLVSRIIVHPNYYDEVNGADIALLELEDPVNLSSHVQPVTLPPASETFP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 CAGSEGHDSCQGDSGGPLVCRVNGTWLQAGVVSWGEGCALPNRPGIYTRVTHYLDWIHQC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 PGMPCWVTGWGDVDNDERLPPPFFLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 KGTRCWVTGWGDVHSGWPLPPPYPLKQVRVPIVENSECDMQYHLGLSTGDNIPIVRDDML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Delta tryptase) (Mast cell
 -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                               SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                         72.2%; Score 1006; DB 1; Length 275; 74.2%; Pred. No. 4.5e-85;
                                                                                                                                                                                                                                                  Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYD_HUMAN STANDARD; PRT; 235 AA. 09B23, 09B23, 09B23, 09B21, 09TD16; 09B23, 09BC22; 09TD16; 09CT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Tryptase delta precursor (RC 3.4.21.59) (Delta tryptase mMCP-7-like) (HmMCP-3-like tryptase III).
                                                                                                                                                                                                                                                                                                                                                                                                    ACC582647FCCB973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               20, Mismatches
                                                                                                                                 MERCES; SOI.144; ...
InterPro; IPRO09003; Cys_Ser_trypsin.
InterPro; IPRO01254; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1A.
Pfam, PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS0040; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                              EMBL; AB038652; BAA93614.1; -.
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275 AA;
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Matches 181; Conserv
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-!- TISSUB SPECIFICITY: Expressed in colon, lung, heart and synovial tissue. May be specific to mast cells.
-!- SIMILARITY: Belongs to peptidase family SI. Tryptase subfamily.
-!- CAUTION: Although Ref.2 reported this as a pseudogene, Ref.4 showed it is expressed and has proteolytic activity when expressed in bacterial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Tryptase is the major neutral protease present in mast cells and is secreted upon the coupled activation-degranulation response of this cell type (By similarity).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but with more restricted specificity than trypsin.
-!- SUBUNIT: Homoterramer (By similarity).
-!- SUBCELLULAR LOCATION: Released from the secretory granules upon mast cell activation (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICATY, AND VARIANT MET-76.
MEDIANE-2258650; PubMed=12391231; Wang H.-W., MCNail H.D., Eusain A., Liu K., Tedla N., Thomas P.S., Raftery M., King G.C., Cai Z.Y., Hunt J.E.;
"Della tryptase is expressed in multiple human tissues, and a recombinant form has protechytic activity.";
J. Immunol. 169:5145-5152(2002).
                                                                                                                                                                                                      MEDIANE=99121069; PubMed=9920877; Pallaoro M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.; "Characterization of genes encoding known and novel human mast cell tryptases on chromosome 16p13.3."; J. Biol. Chem. 274:3355-3362(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16."; Hum. Mol. Genet. 10:339-352(2001).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21096910; PubMed=11157797;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21101554; PubMed=11174199;
Min H.-K., Kambe N., Schwartz L.B.;
"Human mouse mast cell protease 7-like tryptase genes are
                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS ARG-15 AND MET-76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allergy Clin. Immunol. 107:315-321(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9BZJ3-1; Sequence=Displayed;
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EMBL; AF206664; AAG35694.1; -.
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EMBL; AF099147; AAD17861.1; -.
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EMBL: AY055427; AAL17874.1; -.
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HSSP; P20231; 1AAO.
MEROPS; S01.054;
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EMBL; AF318074; AAK12909.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                             NCBI_TaxID=9606;
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PEAM; PF00089; LYPSIN; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
BRART; SM00202; TYP, SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN IS; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE NEG
                                                                                                                                                                                          InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
   Biochemistry 28:4148-4155(1989)
                                                                                                                                               EMBL; M24665; AAA30855.1; -.
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MEROPS; S01.145; -.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89352460; PubMed=2504277; Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.; Molecular cloning of dog mast cell tryptase and a related protease: structural evidence of a unique mode of serine protease activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                     BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

Missing (in isoform 2).

//TId=VSP 008319.

P -> R (in dbSNP:3865205).

//FTId=VAR 016870.

V -> M (in dbSNP:3993987).

//FTId=VAR 016872.

V -> M (in dbSNP:3993987).

//FTId=VAR 016872.

V -> M (in dbSNP:3993987).

//FTIG=VAR 016872.

V -> M (in dbSNP:3993987).

//FTIG=VAR 016872.

V -> S (IN REF. 1; AAD17861).

P -> S (IN REF. 4; AAL17874).

MW; BIFFB6C2A8006B22 CRC64;
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(BY SIMILARITY).
(BY SIMILARITY).
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                        ACTIVATION PEPTIDE (BY SIMILARITY).
TRYPTASE DELTA.
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                                 Pfam: PF00089; trypsin; 1.
Pfam: PF00089; trypsin; 1.
SMRINTS: PR00722; CHYMOTRYPSIN.
SMRAT; SM0000: Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN EBR; 1.
Hydrolase; Serine protease; Signal; Zymogen; Glycoprotein; Alternative splicing; Polymorphism.
SIGNAL 1.
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CHARGE RELAY SYSTEM (1
CHARGE RELAY SYSTEM (1
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Canis familiaris (Dog).
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           InterPro, IPR009003; Cys Ser trypsin.
InterPro, IPR001254; Peptidase S1.
InterPro, IPR001314; Peptidase_SIA.
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Best Local Similarity 84.49
Matches 173; Conservative
Genew; HGNC:14118; TPSD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 PSLIVPPGMLCWVTGWGDIADHTPLPPPYHLQEVEVPIVGNRECNCHYQ--TILEQDDEV 197
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050UL7; 0.000UL7; 0.000UL7; 0.000UL7; 0.000UL7; 0.000UL7; 0.000UL7; 0.000UL7; 0.000UL7; 0.000UL8; 0.000UL7; 0.000UL8; 0.00
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
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-!- FUNCTION: Mast cell protease.
-!- SIMILARITY: Belongs to peptidase family S1
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Best Local
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                                                                                                                                       SEQUENCE FROM N.A. STRAIN=129/Sv, and BALB/c; STRAIN=129/Sv, and BALB/c; MEDLINE=99452974; PubMed=10521469; MODLINE=99452974; PubMed=10521469; Friend D.S., Karlis S.A., Stevens R.L.; Friend D.S., Kralis S.A., Stevens R.L.; "Identification of a new member of the tryptase family of mouse and human mast cell proteages which possesses a novel COOH-terminal
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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(BY SIMILARITY).
(BY SIMILARITY).
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Transmembrane.
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TRYPTASE GAMMA LIGHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
POTENTIAL.
CHARGE RELAY SYSTEM (BY SIMII CHARGE RELAY SYSTEM (BY SIMII CHARGE RELAY SYSTEM (BY SIMII CHARGE RELAY SYSTEM (BY SIMII
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PROSITE; PS55240; TRYPSIN DOM, 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1349391; Tpsgl.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001149; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
                                                                                                           hydrophobic extension.";
J. Biol. Chem. 274:30784-30793(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF175760; AAF03698.1; -. EMBL; AF17523; AAF03696.1; -. EMBL; BC052325; AAH52325.1; -. HSSP; P20231; IAAO.
MEROPS; S01.028; -.
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311
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119 ASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYL 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 RIVGGHAAPAGTWPWQASLRLHK---VHVCGGSLLSPEWVLTAAHCFSGSVNS-SDYQVH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ASADFYPGWQCWVTGWGYTGEGEPLKPPYNLQEAKVSVVDVKTCSQ-----AYNSPNGSL
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                                                                                                                                                                                                                                                                                                                                            Gaps
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"Organization and alternative splicing of CACNAIH.";
"Organization and alternative splicing of CACNAIH.";
"Organization and alternative splicing of Cacanank/DDBJ databases.
Submitted (JAN 2001) to the EMBJ/Genhank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
-!- TISSUE SPECIFICITY: Expressed in many tissues.
-!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which differ by 5 residues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9NRR2; Q9C015; Q9NRR2; G9UBB2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 17-OCT-2001 (Rel. 40, Last annotation update) Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
                            BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                Length 311;
                                                                                                                                                                                                                                                         43.5%; Score 605.5; DB 1; Lengua. 48.6%; Pred. No. 3.1e-48; wiemarches 78; Indels
                                                                                                                                                                                                                   7FC9D6EF6A2A8808 CRC64;
INTERCHAIN (POTENTIAL).
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                                                                                                                                                                                                                   32656 MW;
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                                                                                                                                                                                                                                                                                                                                                121; Conservative
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311 AA;
                                                                                                                                                                                                                                                                                                            Similarity
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151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LREQHLYYQDQLLPVSRIIVHPQFYTAQIG--ADIALLELEEPVKVSSHVHTVTLPPASE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 DFCPGIRCWVTGWGYTREGEPLPPPYSLREVKVSVVDTETCRRD-----YPGPGGSILQP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 DMLCARGP-GDACQDDSGGPLVCQVNGAWVQAGIVSWGEGCGRPNRPGVYTRVPAYVNWI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TFPPGMPCWVIGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYIGDDVRIVRD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 RIVGGHAAPAGAWPWQASLRLRR---MHVCGGSLLSPQWVLTAAHCFSGSLNS-SDYQVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps

    -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.

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M -> V (IN GAMMA-II).

FTIGHAR 012097.

I -> M (IN GAMMA-II).

FTIGHAVR 012099.

S -> T (IN GAMMA-II).

FTIGHOR 012099.

L -> I (IN GAMMA-II).

FTIGHOR 012099.

L -> I (IN GAMMA-II).

FTIGHOR 012010.

L -> F (IN GAMMA-II).

FTIGHOR 012100.

L -> F (IN GAMMA-II).

FTIGHOR 012101.

M -> S (IN REF. 1).

W -> S (IN REF. 1).
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CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                     Pfam; PF00089; trypsin; 1.
PROSTIE: PR00722; CHWOTRYPSIN.
PROSITE: PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN EIS; 1.
PROSITE; PS00135; TRYPSIN EIS; PALSE NEG.
Hydrolase; Serine protes; Signal; Glycoprotein; Zymogen; Transmembrane; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPTASE GAMMA LIGHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
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BY SIMILARITY.
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SIMILARITY.
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                                                                                                                                                                                                                                                         InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                          EMBL; AF191031; AAF76457.1; --
EMBL; AF195508; AAF76458.1; --
EMBL; AF175759; AAF03697.1; --
EMBL; AF175523; AAF03695.1; --
EMBL; AF223663; AAF03695.1; --
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33827 MW;
                                                                                                                                                                                                            HSSP, P007bs, MEROPS, S01.028; -. MEROPS, S01.028; -. Cys. Annew; HGNC:14134; TPSG1.
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Qy 242 HHYV 245
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Search completed: July 22, 2004, 15:23:30 Job time : 54 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 22, 2004, 13:24:46; Search time 98 Seconds (without alignments) 717.901 Million cell updates/sec

US-09-598-982-21

1393 1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP 249 Seguence:

Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\*
geneseqp2004s:\* geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* A\_Geneseq\_29Jan04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	De	AAU12009 Human bet	Human	Human	Recomb		Human	Aau12006	AAU12020 Aau12020 Human bet	Aau12010		AAU12013 Aau12013 Human bet	Aau12018 Human	Aau12021		AAW64240 Aaw64240 Human mas	AAW63175 Human mas	AAU12016 Aau12016 Human bet	Aau12015 Human	AAY55010 Aay55010 Human bet	5 Human	Human	Human	5 Human	Human	
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Aau12024 Human bet Aau12022 Human bet	Human	-		Ade56171 Human Pro		Ade62892 Human Pro	Aaw64237 Human mas	Aaw63173 Human mas	Aaw64242 Murine ma	Aaw63172 Mouse mas		Aaw64239 Gerbil ho	Aaw64233 Murine mM	Aae14343 Human pro	Aaw64234 Rat homol	Ade56169 Rat Prote	Aaw64235 Rat homol	Add47563 Rat Prote
AAU12024 AAU12022	AAW64241	AAW63176	AAU84360	ADE56171	AAE14348	ADE62892	AAW64237	AAW63173	AAW64242	AAW63172	ABB05437	AAW64239	AAW64233	AAE14343	AAW64234	ADE56169	AAW64235	ADD47563
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## ALIGNMENTS

AAU12009 standard; protein; 249 AA. AAU12009; ABU12009

(first entry) 09-APR-2002 

Human beta-II tryptase active site mutant H44A #1.

Human; proteolytic tryptase; protease; recombinant beta-II tryptase; enzyme; mutant; mutein.

Homo sapiens. Synthetic.

WO200198470-A2.

27-DEC-2001.

20-JUN-2001; 2001WO-US019681.

21-JUN-2000; 2000US-00598982.

(PROM-) PROMEGA CORP.

Maffit M, Niles AL, Haak-Frendscho M;

WPI; 2002-114578/15. N-PSDB; AAS20775 DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.

Claim 8; Page 84-85; 126pp; English.

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its

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enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteclytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant human beta-II tryptase active
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                                                                                                                                      100.0%; Score 1393; DB 5; Length 249; 100.0%; Pred. No. 1e-122;
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                                                                                                          Sequence 249 AA;
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these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutain, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for medalling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-luman tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, etc. AAII2009-AAUI2004 represent recombinant human beta-II tryptase active
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                                                                                                                                                                                                                                                                                                                  99.6%; Score 1388; DB 5; Length 249; 99.6%; Pred. No. 3e-122; ive 0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY55011 standard; protein; 249 AA.
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WO200198470-A2.

27-DEC-2001

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This sequence is the human beta-tryptase. The invention relates to a DNA expression construct comprising (5' to 3') a promoter linked to a signal sequence which is linked to a sequence encoding human beta-tryptase. The DNA construct is useful for transforming host cells to express, post translationally process and secrete enzymatically active human tryptase. The method is useful for the production of large amounts of tryptase with defined specifications. The transformant is useful for pharmacological studies, combinatorial library screens and X ray crystallographic studies. The tryptase produced allows for the development of tryptase agonists and/or antagonists, is useful as an antigen to generate allohuman tryptase antibodies in various animals, can be used in screening for compounds which act as tryptase inhibitors, antagonists, and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists etc. may be useful as therapeutics. The tryptase does not require any post-expression or post-parification modifications or manipulations to initiate tryptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity and it has enzymatic activity which compares favourably with cadaveric tryptase. The availability of enzymatically active tryptase facilitates the large scale screening of combinatorial libraries for specific tryptase inhibitors as potential therapeutics and advances the understanding of the biological significance of tryptase in mast cell mediated diseases. The tryptase can be used to detect low levels of
                              expression construct for production of enzymatically active
                                                                                                             Disclosure; Page 43-44; 50pp; English.
                                                   recombinant human beta-tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 249 AA;
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ö RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS 120 ETFPPGMPCWVIGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYIGDDVRIVR 180 DDMLCAGNIRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDW 240 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAAL 60 1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAAL 60 RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS **ETFPPGMPCWVTGWGDVDNDERLPPFFLKQVKVPIMENHICDAKYHLGAYTGDDVRIVR** DDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG1YTRVTYYLDW Gaps .. 0 Length 249; 1; Indels 99.6%; Score 1387; DB 3; 99.6%; Pred. No. 3.7e-122; ive 0; Mismatches 1; 248; Conservative IHHYVPKKP 249 IHHYVPKKP 249 Similarity 241 Query Match Best Local S 61 61 121 181 181 Matches ò ð g à g δ ð

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Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
                                                                       Recombinant human beta-II tryptase.
                 AAU12007 standard; protein; 249 AA
                                                      (first entry)
                                                                                                       enzyme; mutein; mutant
                                                      09-APR-2002
                                    AAU12007;
RESULT 4
       AAU12007
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Homo sapiens

Synthetic.

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The present interaction transcess and the methods for producing these. The mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a bNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its crombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies. The enzymatically-active, generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase intibodies and in drug screening for compounds which act as tryptase inhibitors, antegonists, agonists, ctc. The present sequence represents recombinant human beta-II tryptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS 120
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                                                                                                                                                                                                                                                                                                                                                                                the present invention relates to recombinant human proteolytic tryptases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                      DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                  Haak-Frendscho M;
                                                                                                                                                                                                                                                                                                                                            Claim 60; Page 77-78; 126pp; English.
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                                                                    20-JUN-2001; 2001WO-US019681.
                                                                                                          21-JUN-2000; 2000US-00598982
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                                                                                                                                                                              Maffit M, Niles AL,
                                                                                                                                          (PROM-) PROMEGA CORP
                                                                                                                                                                                                                   WPI; 2002-114578/15.
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Best Local Similarity
                                                                                                                                                                                                                                      N-PSDB; AAS20765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 249 AA;
                                                                                                                                                                                                                                                                                                              site mutation
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RESULT 6

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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic ryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The crive site mutants of proceolytic tryptase provide a rool to investigate the structural and functional properties of the procease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, and antigen active ANU12009-AAU12024 represent recombinant human beta-II tryptase active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                      Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
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Human beta-II tryptase active site mutant S194A #1
                                                                                                                                                                                                                                                                                                                                              Haak-Frendscho M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 90-91; 126pp; English.
                                                                                                                                                                                                                                20-JUN-2001; 2001WO-US019681.
                                                                                                                                                                                                                                                                    21-JUN-2000; 2000US-00598982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.2
Matches 247; Conservative
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                                                            enzyme; mutant; mutein
                                                                                                                                                                                                                                                                                                          (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-114578/15.
N-PSDB; AAS20777.
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                                                                                                                                                      WO200198470-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site mutation.
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                                                                                                                    Synthetic.
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The present invention relates to recombinant human proteclytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence which is operably linked to a secretion signal sequence which is operably linked to a secretion signal sequence which is operably linked to a becretion signal sequence which is operably linked to a becretion signal sequence tryptase with an active site mutation, in hosts transformed to construct drives expression of a mature proteclytic tryptase provide a tool to the cative site mutants of proteclytic tryptase provide a tool to investigate the structural and functional properties of the protease and its companiant proteclytic tryptase produced are useful as an antigen to recombinant proteclytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, applies Adul2009-AAU12024 represent recombinant human beta-II tryptase active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
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                                                                                                                                                           Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
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                                                                                                                       Human beta-II tryptase active site mutant S194A #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haak-Frendscho M;
             AAU12012 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim B; Page 93; 126pp; English.
                                                                                                                                                                                                                                                                                                                                              20-JUN-2001; 2001WO-US019681.
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                                                                                                                                                                              enzyme; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                       (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maffit M, Niles AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS20778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 249 AA;
                                                                                                                                                                                                                                                                         WO200198470-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site mutation
                                                                                                                                                                                                                     sapiens
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                                                                                    09-APR-2002
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                                                                                                                                                                                                                                                                                                           27-DEC-2001
                                                                                                                                                                                                                                      Synthetic.
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                                                   AAU12012;
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AAU12012
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DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
DDMLCAGNTRRDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG1YTRVTYYLDW
                                                                                                                                                            Human; proteolytic tryptase; protease; beta-I tryptase; enzyme.
                                                                                                                                                                                                                                                                                Haak-Frendscho M;
                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 74-75; 126pp; English.
                                                                                          AAU12006 standard; protein; 249 AA.
                                                                                                                                                                                                                             20-JUN-2001; 2001WO-US019681.
                                                                                                                                                                                                                                             21-JUN-2000; 2000US-00598982.
                                                                                                                           (first entry)
                                                241 IHHYVPKKP 249
                                 241 IHHYVPKKP 249
                                                                                                                                           Human beta-I tryptase.
                                                                                                                                                                                                                                                              (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                               Maffit M, Niles AL,
                                                                                                                                                                                                                                                                                               WPI; 2002-114578/15.
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                                                                                                                                                                                             WO200198470-A2.
                                                                                                                                                                                                                                                                                                                                         site mutation.
                                                                                                                                                                             Homo sapiens.
                                                                                                                          09-APR-2002
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181
                                                                                                          AAU12006;
                                                                          RESULT 7
                                                                                   AAU12006
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic cryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its encompainant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc.

The present sequence represents human beta-I tryptase

Claim 8; Page 114-115; 126pp; English.

site mutation.

Sequence 249 AA;

Query Match

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic cryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to construct drives expression of active site mutants of proteolytic tryptase provide a tool to investigate active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its crombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. ANII2024 represent recombinant human beta-II tryptase active

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                                                                     1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAAL
                                         Gaps
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99.2%; Score 1382; DB 5; Length 249; 99.2%; Pred. No. 1.1e-121; ive 0; Mismatches 2; Indels (
                                 247; Conservative
               Local Similarity
                                Matches
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61 RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS 120

1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAAL

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Sequence 249 AA;

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240
for producing enzymatically-inactive proteolytic tryptase, sequence encoding proteolytic tryptase having an active
                                     181 DDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDW
                           ETFPPGMPCWVIGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAY1GDDVRIVR
                                                           DDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPG1YTRVTYYLDW
                                                                                                                                                                                                                          Human, proteolytic tryptase, protease, recombinant beta-II tryptase,
enzyme, mutant, mutein.
                                                                                                                                                                                                           Human beta-II tryptase active site mutant S194A #6
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                                                                                                                                                        AAU12020 standard; protein; 249 AA.
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                                                                                                                                                                                          09-APR-2002 (first entry)
                                                                                              241 IHHYVPKKP 249
                                                                                                              241 IHHYVPKKP 249
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comprises DNA
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Synthetic.
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The enzymatically-active,

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                                                    RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPAS
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                                                                                RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS
                                        LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAAL
                      Gaps
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Length 249;
                    Indels
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 Score 1379; DB 5;
Pred. No. 2.1e-121;
                     1; Mismatches
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98.8%;
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                      246; Conservative
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                                                                                                                                                                                                                                                                                                                                                               Human; proteolytic
           Similarity
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The present invention relates to recombinant human proteclytic tryptases, active site mutants of these tryptases and the methods for producting these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteclytic tryptase with an active site mutation (the construct drives expression of a mature proteclytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteclytic tryptase provide a tool to investigate the structural and functional properties of the protease and its

Claim 8; Page 87-88; 126pp; English.

site mutation

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enzymatic activity, and for modelling studies. The enzymatically-active recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, AAU12009-AAU12024 represent recombinant human beta-II tryptase active
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                                                                                                                         Length 249;
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                                                                                                                         Score 1379; DB 5;
Pred. No. 2.1e-121;
0; Mismatches 2;
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                                                                                                                         Query Match
Best Local Similarity
Matches 247; Conserv
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                                                                                                   Sequence 249 AA;
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these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAUI2009-AAUI2004 represent recombinant human beta-II tryptase active
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Sequence 249 AA;

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                                                                                                                                                                                                                            ETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVR 180
                                                                                                                                                                                                                                                                                                                            DDMLCAGNTRRDSCQGDAGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDW 240
                                                                                                      LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMFFCGGSLIHPQWVLTAAHCVGPDVKDLAAL 60
                                                                             1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAAL 60
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                                              Gaps
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       Length 249;
                                          2; Indels
99.0%; Score 1379; DB 5; 98.8%; Pred. No. 2.1e-121;
                                        1; Mismatches
                                        Matches 246; Conservative
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                       Local Similarity
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AAU12013 standard; protein; 245 AA. 09-APR-2002 AAU12013; RESULT 11 

(first entry)

Human beta-II tryptase active site mutant H44A #2.

Human; proteolytic tryptase; protease; recombinant beta-II tryptase; enzyme; mutant; mutein

Homo sapiens Synthetic. WO200198470-A2

27-DEC-2001.

20-JUN-2001; 2001WO-US019681.

21-JUN-2000; 2000US-00598982

(PROM-) PROMEGA CORP

WPI; 2002-114578/15.

Maffit M, Niles AL,

Haak-Frendscho M;

N-PSDB; AAS20779

20-JUN-2001; 2001WO-US019681

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The present invention relates to recombinant human proteclytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a secretion signal sequence tryptase with an active site mutation (the construct drives expression of a mature proteclytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The active site mutants of proteclytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, compounds which act as tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, all active.
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       DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.
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                                                                                       Claim 40; Page 95-96; 126pp; English.
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Matches 245; Conserv
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tripe site mutants of traces tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a Secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic comprising a mature proteolytic tryptase that lacks enzymatic activity due to the a critic site mutanion, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The critic site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, anteagonists, agonists, etc. AAU12009-AAU12024 represent recombinant human beta-II tryptase active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDW 240
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                                                                                                                                                                                                                                                                                                                     present invention relates to recombinant human proteolytic tryptases,
                                                                                                                                                                                                for producing enzymatically-inactive proteolytic tryptase, sequence encoding proteolytic tryptase having an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAAL
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enzyme, mutant, mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.6%; Score 1374; DB 5; Length 249; 98.8%; Pred. No. 6.2e-121; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta-II tryptase active site mutant H44A #4.
                                                                                                 Haak-Frendscho M;
                                                                                                                                                                                                                                                                             Claim 8; Page 109-110; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU12021 standard; protein; 245 AA.
                  21-JUN-2000; 2000US-00598982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 98.8
Matches 246; Conservative
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                                                        (PROM-) PROMEGA CORP.
                                                                                               Niles AL,
                                                                                                                                      WPI; 2002-114578/15
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                                                                                                                                                         N-PSDB; AAS20784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 249 AA;
                                                                                                                                                                                                  construct
                                                                                                                                                                                                                                        site mutation.
                                                                                                                                                                                                                   comprises DNA
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                                                                                               Maffit M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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The present invention relates to recombinant manam procession control of these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic cryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the cative site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatic activity, and for modelling studies. The enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant human beta-II tryptase active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to recombinant human proteolytic tryptases,
                                                                                                                                                                                                                                                                                                                                                                              DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVGGQBAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                Haak-Frendscho M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 40; Page 117-118; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU12008 standard; protein; 245 AA.
                                                                                                                                                            20-JUN-2001; 2001WO-US019681.
                                                                                                                                                                                                    21-JUN-2000; 2000US-00598982
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                                                                                                                                                                                                                                                                                Maffit M, Niles AL,
                                                                                                                                                                                                                                          (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                        WPI; 2002-114578/15
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                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS20787
                                                                              WO200198470-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         site mutation
                     Homo sapiens.
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                                                                                                                      27-DEC-2001
                                        Synthetic.
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AAU12008
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us-09-598-982-21.rag

245 VPKKP 249

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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the procease and its encommant of the structural and for modelling studies. The enzymatically-active, compounds which act as tryptase and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, compounds which act as tryptase inhibitors, antagonists, agonists, the present sequence represents recombinant human mature beta-II tryptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
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                                                                                                                              Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
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                                                                                        Recombinant human mature beta-II tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Haak-Frendscho M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 61; Page 80; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                            21-JUN-2000; 2000US-00598982.
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                                                       (first entry)
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Best Local Similarity 99.67
Matches 244; Conservative
                                                                                                                                                   enzyme; mutein; mutant
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N-PSDB; AAS20766.
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                                                                                                                                                                                                                                              WO200198470-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site mutation.
                                                                                                                                                                                         Homo sapiens.
                                                       09-APR-2002
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                                                                                                                                                                                                          Synthetic.
                   AAU12008;
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This is the deduced amino acid sequence of human mast cell tryptase compositions comprising an isolated tryptase-7 that may include chimeric proteins that contain (a) a human tryptase for all but the active site region and (b) the substrate-binding pocket of mouse tryptase-7 or its homologues (see human active that codes for a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product, to decrease fibrinogen activity; a nucleic acid encoding a product, to decrease fibrinogen activity; a nucleic acid encoding a serine protease (SP); and a method of producing a mature SP by expressing the inactive zymogen in a host cell, and cleaving the enterokinase susceptibility domain. The tryptase-7 polypeptides can be used to treat disorders mediated by undestrable thrombus clot formation such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial infarction and reocclusion following angioplasty of blood clots associated with pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal vein and peripheral arterial thrombosis. They are also useful for all surgical procedures that require decreased blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compositions containing tryptase-7, e.g. mouse mast cell protease-7 are used to treat clot formation in e.g. myocardial infarction, reocclusion following angioplasty or pulmonary thrombo-embolism.
                                                                                                                                                                                                                          Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7; blood clot; anticoagulant; myocardial infarction; reocclusion; thromboembolism; cerebral embolism; thrombosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 66-67; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                   1. .18
/label= Sig_peptide
19. .28
/label= Pro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    29. .274 ___ /label= Mat_protein
                                                                                        AAW64240 standard; protein; 274 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                             Human mast cell tryptase II/beta.
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   241 VPKKP 245
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                                                                                                                                                             24-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                       RESULT 15
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Gaps

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Query Match 98.2%; Score 1368; DB 2; Length 274; Best Local Similarity 99.6%; Pred. No. 2.6e-120; Matches 244; Conservative 0; Mismatches 1; Indels 0

Sequence 274 AA;

181

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Gaps

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OY 5 IVGGGEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL 64

DD 30 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL 89

CY 65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFF 124

DD 90 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFF 149

CY 125 PGMPCWVTGWGDVDNDBRLPPFPLKQVKVPIMBNHICDAKYHLGAYTGDDVRIVRDDML 184

DD 150 PGMPCWVTGWGDVDNDBRLPPFPLKQVKVPIMBNHICDAKYHLGAYTGDDVRIVRDDML 209

CY 185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 249

DD 210 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 269

CY 245 VPKKP 249

DD 270 VPKKP 274
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Search completed: July 22, 2004, 15:22:25 Job time : 100 secs

us-09-598-982-21.rai

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Page

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 22, 2004, 15:20:41; Search time 58 Seconds (without alignments) 221.636 Million cell updates/sec Run on:

US-09-598-982-21

1 LEKRIVGGQEAPRSKWPWQV......IYTRVTYYLDWIHHYVPKKP 249 1393 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues Searched:

389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgr2\_6/ptcdata/2/iaa/5A COMB.pep:\*
2: /cgn2\_6/ptcdata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptcdata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptcdata/2/iaa/PCTUG COMB.pep:\*
6: /cgn2\_6/ptcdata/2/iaa/PCTUG COMB.pep:\* Issued\_Patents\_AA:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	-079-970A-5 Sequence 5, Appl.	-970A-6 Seguence 6,	Sequence 1,	21,	04B-16 Sequence 16,	-366A-19 Sequence 19,	04B-14 Sequence 1	4, 4	601-318-5	501-318-6 Sequence 6,	601-318-7 Sequence 7,	23	18	944-483-69 Sequence 69	016-366A-17 Sequence 17	Sequence 12	-366A-15 Sequence 15	978-404B-21 Sequence 21	978-404B-8 Sequence	978-404B-3 Sequence 3,	978-404B-5 Sequence 5,	978-404B-6 Sequence 6,	4	4	430-854-4	845-998-6 Seguence 6,	
	-60-SD	-09	0	0	US-08-	- 09	US-08-	-09	-60-SD	-60~SD	-60-SD	-60-SN	-80-SN	US-08-	-60-SD	US-08-	-0	US-08-	US-08-	US-08-	US-08-	US-08-	US-08-	-60-SD	-60-SD	US-08-	
DB		m	4	0	7	7	Ŋ	4	4	4	4	Ŋ	7		•	(1			ď							(7	
Length	249	4	245	274	274	273	273	244	244	244	244	267	267	245	275	275	276	276	270	273	274	273	190	190	190	190	
% Query Match	9.66	98.2	98.2	98.2	98.2	•	97.8	•		7.	97.7	96.5		Н		91.5	78.3	78.3	77.2	75.7	75.4	74.4	50.4	50.4			
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Result No.	н	2	m	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	

Sequence 6, Appli Sequence 10, Appl	7	6	Sequence 7, Appli	6	12,	Sequence 11, Appl	Sequence 66, Appl	Sequence 7, Appli	Sequence 263, App		Sequence 263, App	Sequence 4, Appli	Sequence 3, Appli	Sequence 257, App	257,	Sequence 257, App
US-09-430-854-6 US-08-978-404B-10	US-09-386-653A-7	US-09-386-653A-9	US-09-387-375-7	US-09-387-375-9	US-09-386-642-12	US-09-386-642-11	US-08-944-483-66	US-09-386-629-7	US-09-907-794A-263	US-09-905-125A-263	US-09-902-775A-263	US-09-023-942A-4	US-09-008-271A-3	US-09-907-794A-257	US-09-905-125A-257	US-09-902-775A-257
m 7	4	4	4	4	4	4	3	4	4	4	4	4	٣	4	4	4,
190	290	315	284	316	319	328	299	317	317	317	317	312	314	314	314	314
50.1	40.5	39.8	38.5	37.9	36.4	36.4	36.3	36.0	36.0	36.0	36.0	35.9	35.4	35.4	35.4	35.4
698 684.5	563.5	554.5	536.5	527.5	507	507	206	501.5	501.5	501.5	501.5	499.5	493.5	493.5	493.5	493.5
28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1387; DB 3; Length 249; 99.6%; Pred. No. 5.5e-141; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
                                            Sequence 5, Application US/09079970A Patent No. 6274366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.6'
Matches 248; Conservative
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                                                                                            GENERAL INFORMATION:
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                        US-09-079-970A-5
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RESULT 1
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Gaps .,

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61 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CAGNTREDSCQGDSGGPLVCKVNGTWLQAGVVSWGGGCAQPNRPGIYTRVTYYLDWIHHY 240
121 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 180
                                                                                  181 CAGNTRRDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 240
                                            185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
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Pred. No. 5.9e-139;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissensch. e.V APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bundschub, Daniela
APPLICANT: Benne, Rolf
APPLICANT: Geebel, Karl-Josef
TITLE OF INVENTION: Trypcase-Inhibitoren
FILE REFERENCE: 17674P WO-1
CURRENT APPLICATION NUMBER: US/09/601,318
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: DE19804761.4
PRIOR PILING DATE: 1998-010
                                                                                                                                                                                                                                                                                                                                                                                                              Moroder, Luis
Pereira, Pedro Jose Barbosa
Bergner, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huber, Robert
Sommerhoff, Christian
Schaschke, No. 6613769bert
                                                                                                                                                                                                                                                                              Sequence 1, Application US/09601318
Patent No. 6613769
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Ulrich, Wolf-Rdiger
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Thibaut, Ulrich
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SEQ ID NO 1
LENGTH: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.6
Matches 244; Conservative
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Martin, Thomas
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                                                                                                                                                                         241 VPKKP 245
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                                                                                                                               245 VPKKP 249
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                               RVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS 120
                                                                                                               ETFPPGMPCWVTGMGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVR 180
                                                                                                                                                                                                  181 DDM.CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                       ETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVR 180
                                                                                                                                                                            DDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDW 240
    RVQLREGHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPAS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Fatentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/079,970A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.2%; Score 1368; DB 3;
99.6%; Pred. No. 5.9e-139;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Intellectual Property Department
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY FAGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCRET NUMBER: 34506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2106
TELEPAX: (608) 831-2106
TELEPAX: (608) 831-2106
TELEPAX: (608) 831-2106
SEQUENCE CHARACTERISTICS:
FROGRAFI 245 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09079970A Patent No. 6274366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 244; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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          Sequence 21. Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                          COUNTRY: 0.2...
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
PTI.NG DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
APPLICATION NUMBER: 60/037,090
ATTORNEY AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE JOCKET NUMBER: 80801/7093
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 274 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear 16-3623 ...
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90 REQHLYYODOLLPVSRIIVHPOFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 149
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                    Sequence 16, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL.PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PESTERN: DOS
SOFTWARE: PESTERE FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-016-366A-19; Sequence 19, Application US/09016366A; Patent No. 5955431
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                                                                                                                                                                                                                      STREET: 600 Atlantic Avenue
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/03
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 amino acids
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Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-978-404B-16
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                                                                                                                                                                                                                                                                    STATE:
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Wolf, Greenfield & Sacks, P.C.
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TITLE OF INVENTION: FIBRINGEN
                                                                    600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: No. 5968782e
                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                    CORRESPONDENCE ADDRESS:
                                                                                                                         COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                            STREET: 600 ---
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                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-978-404B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.8%; Score 1363; DB 2;
99.2%; Pred. No. 2.4e-138;
tive 0; Mismatches 2;
               APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OP INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION. 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: PLUMEY, Blizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                         ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08978404B Patent No. 5968782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: 273 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.23
Matches 243; Conservative
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                                                                                                                                                                                                               ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-720-2441
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                                                                                                                                                                                                   U.S.A.
GENERAL INFORMATION:
                                                                                                                                              STREET: 600 A
CITY: Boston
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TOPOLOGY:
US-09-016-366A-19
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US-08-978-404B-14
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                                                                                                                                                               CITY:
STATE:
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Richard L. MAST CELL PROTEASE THAT CLEAVES

APPLICANT: Stevens, TITLE OF INVENTION:

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89 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFP 148
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APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissensch. e.V
APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
APPLICANT: Bode, Wiltam
APPLICANT: Moroder, Luis
APPLICANT: Pereira, Pedro Jose Barbosa
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-318-5
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LENGTH: 244
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APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissensch. e.V
APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
APPLICANT: Bode, Wolfram
APPLICANT: Bode, Wolfram
APPLICANT: Borer, Pedro Jose Barbosa
APPLICANT: Berger, Andreas
APPLICANT: Berger, Andreas
APPLICANT: Berger, Robert
APPLICANT: Sommerhoff, Christian
APPLICANT: Schaschke, No. 6613769bert
APPLICANT: Schaschke, No. 6613769bert
                                                                                                                     APPLICANT:

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PRIOR APPLICATION NUMBER: DE19804761.4
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCHING VET. 2.1
SEQ ID NO 4
LENGTH: 244
                      Huber, Robert
Sommerhoff, Christian
Schaschke, No. 6613769bert
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Patent No. 6613769
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Martin, Thomas
Stadlwieser, Josef
Ulrich, Wolf-Rdiger
Dominik, Andreas
Bergner, Andreas
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Best Local Similarity 99.6
Matches 243; Conservative
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ORGANISM: Homo sapiens
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181 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 240
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APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissensch. e.V
APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
APPLICANT: Thibaut, Ulrich
APPLICANT: Bundschub, Daniela
APPLICANT: Beune, Rolf
APPLICANT: Geobel, Ral-Josef
ITLE OF INVENTION: Tryptase-Inhibitoren
FILE REFERENCE: 17674 WO-1
CURRENT APPLICATION NUMBER: US/09/601,318
CURRENT FILING DATE: 2001-01-22
PRIOR PLLING DATE: 1998-02-06
PRIOR PLLING DATE: 1998-02-06
PRIOR FILING DATE: 1998-11-06
NUMBER OF SQL ID NOS: 7
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TITLE OF INVENTION: Tryptase-Inhibitoren
FILE REFERENCE: 17674P WO-1
FURENT APPLICATION NUMBER: US/09/601,318
CURRENT FILING DATE: 2001-02
PRIOR APPLICATION NUMBER: DE19804761.4
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Moroder, Luis
Pereira, Pedro Jose Barbosa
Bergner, Andreas
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Sommerhoff, Christian
Schaschke, No. 6613769bert
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Martin, Thomas
Stadlwieser, Josef
Ulrich, Wolf-Rdiger
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APPLICANT: Beume, Rolf
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Thibaut, Ulrich
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Best Local Similarity 99.6'
Matches 243; Conservative
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61 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 120
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                                                                                                                                                                                                                                                                                        125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                                                                       185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                                                                                1 IVGGQEAPRSKWPWQVSLRVHGPYMMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQL 60
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                                                                                     Gaps
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                                            Length 244;
                                                                                     Indels
                                          Score 1361; DB 4;
Pred. No. 3.3e-138;
0; Mismatches 1;
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APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
SUFTWARENT APPLICATION DATE: US/09/016,366A
FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 23, Application US/09016366A; Patent No. 5955431
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                            97.78;
99.68;
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                                                                                     Conservative
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ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                            Query Match
Best Local Similarity
Matches 243; Conserv
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STREET: 60
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      US-09-601-318-7
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                                                                                                                                                                                                                               Length 244;
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                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                          Score 1361; DB 4;
Pred. No. 3.3e-138;
0; Mismatches 1;
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APPLICANT: Beume, Rolf
APPLICANT: Goebel, Karl-Josef
TILE OF INVENTION: Tryptase-Inhibitoren
FILE SPERENCE: 17674P WO-1
CURRENT APPLICATION NUMBER: US/09/601,318
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PRIOR APPLICATION NUMBER: DE19804761.4
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: DE19851300.3
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-02-06
PRIOR PAPLICATION NUMBER: DE19851300.3
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 244
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Huber, Robert
Sommerhoff, Christian
Schaschke, No. 6613769bert
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Patent No. 6613769
GENERAL INFORMATION:
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Ulrich, Wolf-Rdiger
Dominik, Andreas
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Best Local Similarity 99.6
Matches 243; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
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Martin, Thomas
                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-09-601-318-6
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ORGANISM: Homo sapiens
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T: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 69, Application US/08944483 Patent No. 6232456
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APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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TELECOMMUNICATION : TELEPHONE: 847/935-1729
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US-08-944-483-69
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IBM Compatible
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: COHEN,
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US-08-944-483-69
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APPLICANT:
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                                                                                                                                     REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                          83 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 142
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                                                       5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/08978404B
Patent No. 5968782
GENERAL INFORTION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
Pred. No. 2.5e-136;
0; Mismatches 4;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY-AGENT INFORMATION:
NAME: Plumer, Blizabeth R.
REGISTRATION NUMBER: 36,637
RESTERNCE/DOCKET NUMBER: 36,637
RESTERNCE/DOCKET NUMBER: B0801/7090
TELEROMMUNICATION INFORMATION:
NAME: Plumer, Blizabeth R.
REGISTRATION NUMBER: 36,637
RESTERNCE/DOCKET NUMBER: B0801/7090
TELEROMMUNICATION INFORMATION:
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al Similarity 98.4%;
241; Conservative
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Best Local Similarity 98.4
Matches 241; Conservative
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ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-978-404B-18
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STREET: 60
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NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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                                                                                       65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                            83 REQHLYYQDQLLPVSRIIVHDQFYTAQIGADIALLELEEBVKVSSHVHTVTLPPASETFP
                                                                                                                                                                                                                                                                                               143 PGMPCWVIGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML
23 IVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML
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121 PGMPCWVTGWGDVDNDEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDML 180
                                                                                                                                                                                                                                                                                                                                                 181 CAGNSQRDSCKGDSGGPLVCKVNGTWLQAGVVSWDEGCAQDNRPGIYTRVTYYLDWIHHY 240
                                                                                                                                                              REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                       61 REQHLYYQDQLLPVSRIIVHPQFYIIQTGADIALLELEBPVNISSRVHTVMLPPASETFP 120
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                                                                                                               1 IVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHCLGPDVKDLATLRVQL
                                                                              5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                        Gaps
                                     0,
  Length 245;
                                        Indels
Score 1274; DB 3;
Pred. No. 7.5e-129;
6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENTING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Wolf, Greenfield & Sacks, P.C. 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09016366A Patent No. 5955431 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
                  Best_Local Similarity 92.2
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617-720-350
TELEFAX: 617-720-2441
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STRANDEDNESS: sin
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US-09-016-366A-17
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91.5%; Score 1274; DB 2; Length 275;

Query Match

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                                                                                                                                               91 REQHLYYQDQLLPVSRIIVHPQFYIIQTGADIALLELEEPVNISSRVHTVMLPPASETFP 150
                                                                                                                                                                                                                   244
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                                                                                                                        65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                  125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
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                                                                         11 IVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHCLGPDVKDLATLRVQL
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                                                  5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                0; Gaps
                Indels
                  13;
92.2%; Pred. No. 8.8e-129;
                6; Mismatches
                Matches 226; Conservative
Best Local Similarity
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Search completed: July 22, 2004, 15:27:27 Job time : 59 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July 22, 2004, 15:25:12; Search time 940 Seconds (without alignments) 82.953 Million cell updates/sec Run on:

US-09-598-982-21 1393 1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP 249 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameters:

1288442 segs, 313154207 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

(cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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(cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
(cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 74, Appl	74.	74	74.	92.		92.	92,	104,	104,	104,	104	44	44.	
QI	US-10-150-813-74	US-10-139-854-74	US-10-131-409-74	US-10-150-811-74	US-10-150-813-92	US-10-139-854-92	US-10-131-409-92	US-10-150-811-92	US-10-150-813-104	US-10-139-854-104	US-10-131-409-104	US-10-150-811-104	US-09-813-432-44	US-10-246-583-44	US-10-352-684A-48
	12	12	14	15	12	12	14	15	12	12	14	15	10	12	15
% Query Match Length DB	254	254	254	254	256	256	256	256	264	264	264	264	275	275	275
% Query Match	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2	98.2
Score	1368	1368	1368	1368	1368	1368	1368	1368	1368	1368	1368	1368	1368	1368	1368
Result No.	1	8	3	4	S	9	7	80	თ	10	11	12	13	14	15

SOFTWARE: Patentin Ver. 2; SEQ ID NO 74; LENGTH: 254; TYPE: PRT
CORGANISM: Homo sapiens
US-10-150-813-74

Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appl	Appl	Appl	App1	Appli
44,	94,	44	92,	40,	13,	90,	84,	84,	84,	84,	88	36,	46,	52,	98,	98	98	98	42,	42,	42,	42,			86,				
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-174-364-44	-10-287-2	-689-832-4	ò		'n	US-10-287-226-90	US-10-150-813-84	-139-854-8	-10-1	-10-150-811-8	10-287-226-8	10-117-	10-352-684A-4		-813 - 9	-10-139-854-9	US-10-131-409-98	10-150-811-9	09-813-	-10-246-583-4	US-10-174-364-42	-10-689-8	-10-117-323-3	-10 - 311 - 9	-10-150-813-8	4-8	-131-40	US-10-150-811-86	US-10-275-505-8
15	16	16	16	14	16	16	12	17	14	15	16	14	15	10	12	17	14	15	10	17	15	16	14	14	12	12	14	15	91
275	275	275	275	272	691	275	266	266	266	266	279	275	275	231	199	199	199	199	252	252	252	252	276	276	247	247	247	247	310
98.2	98.2	98.2	97.8	7.96	95.4	95.0	94.5	94.5	94.5	94.5	94.2	91.5	91.5	91.2	79.3	79.3	79.3	79.3	78.3	78.3	78.3	78.3		•	76.4	76.4	76.4	76.4	75.7
1368	1368	1368	1363	1347.5	1329	1323	1317	1317	1317	1317	1312	1274	1274	1270	1104	1104	1104	1104	1091	1001	1001	1001	1001	1077	1064	1064	1064	1064	1054
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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PRIOR APPLICATION NUMBER: 09/899,954
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR PLING DATE: 2001-07-03
PRIOR PELICATION NUMBER: 60/182,733
PRIOR APPLICATION NUMBER: 60/183,896
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR PLING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR APPLICATION NUMBER: 60/184,482
PRIOR APPLICATION NUMBER: 60/184,482
PRIOR PLING DATE: 2000-08-10
PRIOR PLING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,744
PRIOR PLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/184,744
PRIOR APPLICATION NUMBER: 60/184,745
                                                                                                                                                                 APPLICANT: Majumder
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CIPICON2
CURRENT APPLICATION NUMBER: US/10/150,813
CURRENT FILING DATE: 2002-12-03
Sequence 74, Application US/10150813 Publication No. US20030224367A1 GENERAL INFORMATION:
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RESULT 3
US-10-131-409-74
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Sequence 74, Application US/10139654

Sequence 74, Application US/10139654

Sequence 74, Application No. 1020030202971A1

SEQUENCE 10 No. 1020030202971A1

SEXEMATION NO. 10200202971A1

TITLE OF INVENTION: NO. 1020020297

CURRENT FILING DATE: 15966-675C002

PRIOR APPLICATION NUMBER: 09/783,429

PRIOR APPLICATION NUMBER: 09/783,429

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR APPLICATION NUMBER: 60/182,734

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR APPLICATION NUMBER: 60/184,497

PRIOR APPLICATION NUMBER: 60/184,482

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR PILING DATE: 2000-08-10

PRIOR PILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: 60/197,083

PRIOR APPLICATION NUMBER: 60/197,083

PRIOR APPLICATION NUMBER: 60/133,405

PRIOR APPLICATION NUMBER: 60/133,405

PRIOR APPLICATION NUMBER: 60/133,405

PRIOR APPLICATION NUMBER: 60/133,405

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR APPLICATION NUMBER: 60/197,083

PRIOR APPLICATION NUMBER: 60/197,083

PRIOR APPLICATION NUMBER: 60/184,744

PRIOR APPLICATION NUMBER: 60/184,744
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     Length 254;
                                                    1; Indels
  Score 1368; DB 12;
Pred. No. 1.5e-124;
                                                    0; Mismatches
98.2%;
                                                    Matches 244; Conservative
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ORGANISM: Homo sapiens
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                             Best Local Similarity
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     Query Match
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APPLICANT: Malyankar et al.
TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CIP1CON1
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CURRENT APPLICATION NUMBER: 05/089,54

PRIOR APPLICATION NUMBER: 05/089,54

PRIOR FILING DATE: 2002-10-24

PRIOR FILING DATE: 2001-07-03

PRIOR PLICATION NUMBER: 60/182,733

PRIOR PLING DATE: 2000-02-15

PRIOR PLING DATE: 2000-02-15

PRIOR PLING DATE: 2000-02-15

PRIOR PLING DATE: 2000-02-23

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-03-13

PRIOR PLING DATE: 2000-03-13

PRIOR PLING DATE: 2000-03-14

PRIOR PLING DATE: 2000-09-18

PRIOR PLING DATE: 2000-09-18
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Matches 244; Conservative
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RESULT 4 US-10-150-811-74

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                                                                                                                                                APPLICANT: Majumder
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CIPICON2
CURRENT APPLICATION NUMBER: 105.10/150,813
CURRENT FILING DATE: 2002-12-03
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Publication No. US20030202971A1
GENERAL INFORMATION:
APPLICANT: Majunder, Kumud
ITILE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CON2
CURRENT APPLICATION NUMBER: US/10/139,854
CURRENT FILING DATE: 2002-12-02
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Remaining Prior Application data removed - See File Wrapper or PALM.
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PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-15
PRIOR PILING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-23
PRIOR PILING DATE: 2000-02-23
PRIOR PELING DATE: 2000-02-13
PRIOR PILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-17
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                                     Sequence 92, Application US/10150813
Publication No. US20030224367A1
GENERAL INFORMATION:
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Matches 244; Conservative
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US-10-150-813-92
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US-10-139-854-92
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TITLE OF INVENTION: No. US20040010120A1e1 Polypeptides and Nucleic Acids Encoding Sam
FILE REPERNER: 15966-675CTP2CON1
CURRENT APPLICATION WUMBER: US/10/150,811
CURRENT FILING DATE: 2002-05-17
PRIOR PAPLICATION NUMBER: 06/182,733
PRIOR APPLICATION NUMBER: 06/182,733
PRIOR APPLICATION NUMBER: 60/182,733
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR FILING DATE: 2000-02-15
PRIOR PRIOR DATE: 2000-02-22
PRIOR PELIOR DATE: 2000-02-22
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190 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 249
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Publication No. US20040010120A1
GENERAL INFORMATION:
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Best Local Similarity 99.6
Matches 244; Conservative
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US-10-150-811-74
                                                                                                              245 VPKKP 249
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2 ID NO 74 LENGTH: 254

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APPLICANT: Malyankar et al.
TITLE OF INVENTION: No. US20040010120Alel Polypeptides and Nucleic Acids Encoding Same File Reference: 15966-67SCIP2CON1
CURRENT APPLICATION NUMBER: US/10/150,811
CURRENT FILING DATE: 2002-05-17
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                                                                 PRIOR AFFLIANTON NUMBER: 60/184,482
PRIOR APPLICATION NUMBER: 60/184,482
PRIOR APPLICATION NUMBER: 60/184,744
PRIOR PLING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/194,744
PRIOR APPLICATION NUMBER: 60/197,083
PRIOR PELING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/233,405
PRIOR FILING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PALENTIN Ver. 2.1
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PRIOR APPLICATION NUMBER: 09/970, 607
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/182,733
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR APPLICATION NUMBER: 60/183,896
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR APPLICATION NUMBER: 60/224,157
PRIOR APPLICATION NUMBER: 60/224,157
PRIOR APPLICATION NUMBER: 60/244,157
PRIOR PILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
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APPLICATION NUMBER: 60/197,083
FILING DATE: 2000-04-13
                                              APPLICATION NUMBER: 60/224,157
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           FILING DATE: 2000-02-23
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Best Local Similarity 99.6'
Matches 244; Conservative
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CRGANISM: Homo sapiens
US-10-131-409-92
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Publication No. US20030199465A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: No. US20030199465A1e1 Polypeptides and Nucleic Acids Encoding Sammarent September 15966-675CIPICON1
CURRENT APPLICATION NUMBER: US/10/131,409
CURRENT FILING DATE: 2002-10-24
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PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/182,733
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR FILING DATE: 2000-02-15
PRIOR PILING DATE: 2000-02-22
PRIOR PLICATION NUMBER: 60/183,896
PRIOR PLICATION NUMBER: 60/184,497
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R FILING DATE: 2000-08-10
R APPLICATION NUMBER: 60/184,482
RR FILING DATE: 2000-02-23
RR FILING DATE: 2000-02-24
RR APPLICATION NUMBER: 60/184,744
RR FILING DATE: 2000-02-4
RR APPLICATION NUMBER: 60/197,083
RR FILING DATE: 2000-04-13
RR APPLICATION NUMBER: 60/233,405
RR FILING DATE: 2000-09-18
APPLICATION NUMBER: 09/783,429
FILING DATE: 2001-02-14
APPLICATION NUMBER: 60/182,733
FILING DATE: 2000-02-15
APPLICATION NUMBER: 60/182,724
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APPLICATION NUMBER: 60/183,896
FILING DATE: 2000-02-22
APPLICATION NUMBER: 60/184,497
FILING DATE: 2000-02-23
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Best Local Similarity 99.6
Matches 244; Conservative
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ORGANISM: Homo sapiens
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     US-10-150-813-104
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TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675CTPICON2
CURRENT APPLICATION NUMBER: US/10/150,813
FRIOR APPLICATION NUMBER: 09/898,954
PRIOR FILING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-08-10
PRIOR PAPLICATION NUMBER: 60/184,497
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR PLING DATE: 2000-08-10
PRIOR PLING DATE: 2000-08-10
PRIOR PLING DATE: 2000-09-14
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-09-18
PRIOR PRIOR APPLICATION NUMBER: 60/184,744
PRIOR FILING DATE: 2000-09-18
PRIOR PRIOR APPLICATION NUMBER: 60/194,083
PRIOR PLING DATE: 2000-09-18
PRIOR PRIOR PAPIL CATION NUMBER: 60/197,083
PRIOR PLING DATE: 2000-09-18
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                       PRIOR FILING DATE: 2000-09-18
Remaining Frior Application data removed - See File Wrapper or PALM
WUMBER OF SEQ ID NOS: 138
SOFTWARE: PATENTIN VEY: 2.1
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Publication No. US20030224367A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/233,405
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SEQ ID NO 104
LENGTH: 264
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                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens
US-10-150-811-92
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ORGANISM: Homo sapiens
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                                                                                                                 SEQ ID NO 92
LENGTH: 256
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Best Local S
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CURRENT APPLICATION: NOVEL POlypeptides and Nucleic Acids Encoding Same
FILE REPERBUCE: 1596-675CON2
CURRENT APPLICATION NUMBER: 06/12/139,854
FRIOR APPLICATION NUMBER: 09/783,429
FRIOR APPLICATION NUMBER: 06/182,733
FRIOR PILING DATE: 2000-02-15
FRIOR APPLICATION NUMBER: 60/182,724
FRIOR APPLICATION NUMBER: 60/182,724
FRIOR APPLICATION NUMBER: 60/184,497
FRIOR APPLICATION NUMBER: 60/184,497
FRIOR APPLICATION NUMBER: 60/184,497
FRIOR APPLICATION NUMBER: 60/184,497
FRIOR APPLICATION NUMBER: 60/184,482
FRIOR APPLICATION NUMBER: 60/184,744
FRIOR FILING DATE: 2000-02-24
FRIOR FILING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: 60/184,744
FRIOR PLING DATE: 2000-02-24
FRIOR PLING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: 60/197,083
FRIOR PLING DATE: 2000-04-13
FRIOR FILING DATE: 2000-04-13
FRIOR FILING DATE: 2000-04-13
FRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                 20 IVGGQEAPRSKWPWQVSLRVHGPYWMFFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQL
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                                                                                                                                                             5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                     Gaps
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Publication No. US20030202971A1
GENERAL INFORMATION:
APPLICANT: Majumder, Kumud
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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    DB 12; Length 264;
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98.2%; Score 1368; DB 12; 99.6%; Pred. No. 1.6e-124;
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                                                                                 0; Mismatches
                                                                            Matches 244; Conservative
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SEQ ID NO 104
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US-10-139-854-104
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QY         185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244           DD         200 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 259           QY         245 VPKKP 249	Db 260 VPKKP 264	RESULT 12 US-10-150-811-104 ; Sequence 104, Application US/10150811 · Dublication No. HR200400112081	GENERAL INFORMATION: ; APPLICANT: Malyankar et al. ; TITLE OF INVENTION: No. US20040010120Alel Polypeptides and Nucleic Acids Encoding ; FILE REFERENCE: 15966-675CIP2CON1	; CURRENT APPLICATION NUMBER: US/10/150,811 ; CURRENT FILING DATE: 2002-05-17 ; PRIOR APPLICATION NUMBER: 09/970,607 ; PRIOR FILING DATE: 2001-10-03 ; PRIOR APPLICATION NUMBER: 60/182,733 ; PRIOR FILING DATE: 2000-02-15 ; PRIOR FILING DATE: 2000-02-25 ; PRIOR FILING DATE: 2000-02-22 ; PRIOR FILING DATE: 2000-02-22		FRIOR APPLICATION NUMBER: 60/233,405  FRIOR PLIING DATE: 2000-09-18  FREMAINING PATE: 2000-09-18  SOFTWAREN OF SEQ ID NOS: 138  SOFTWAREN PATENT Ver. 2.1  SEQ ID NO 104  LENGTH: 264  TYPE: PRT  TYPE: PRT  CORDANISM: Homo sapiens	Query Match 98.2%; Score 1368; DB 15; Length 264; Best Local Similarity 99.6%; Pred. No. 1.6e-124; Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 5 IVGGQBAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL 64 	OY 65 REQHLYYQDQLLPVSRIIVHPQPYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124	OY 125 PGMPCWVJGWGDVDNDERLPPPPPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184	185 CAGNTF        200 CAGNTF	QY 245 VPKKP 249        DD 260 VPKKP 264
	125 FGARCWYIGWGDVDDAUEKLEFFERAXVKVETMENHICDAKIRIGGDVKIVKDDML 184  [40] FGWECWYIGWGDVDNDERLEPPFELKQVKVEIMENHICDAKYHLGAYIGDDVRIVRDDML 199	185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244 200 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 259	245 VPKKP 249        260 VPKKP 264	TRESULT 11  US-10-131-409-104  1 Sequence 104, Application US/10131409  2 Sequence 104, Application US/10131409  3 GENERAL INFORMATION:  3 APPLICANT: MalYankar et al.  3 TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding  4 TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding  5 TITLE REPERENCE: 15966-675CIPICONI  6 CURRENT APPLICATION NUMBER: US/10/131,409  6 CURRENT APPLICATION NUMBER: 2002-10-24	PRIOR APPLICATION NUMBER: 09/898,954  PRIOR FILING DATE: 2001-07-03  PRIOR FILING DATE: 2000-02-15  PRIOR FILING DATE: 2000-02-15  PRIOR APPLICATION NUMBER: 60/182,724  PRIOR APPLICATION NUMBER: 60/183,896  PRIOR FILING DATE: 2000-02-15  PRIOR FILING DATE: 2000-02-15  PRIOR FILING DATE: 2000-02-15  PRIOR APPLICATION NUMBER: 60/183,896  PRIOR APPLICATION NUMBER: 60/184,497	PRIOR FILING DATE: 2000-02-23  PRIOR APPLICATION NUMBER: 60/224,157  PRIOR FILING DATE: 2000-08-10  PRIOR FILING DATE: 2000-02-23  PRIOR PILING DATE: 2000-02-23  PRIOR PILING DATE: 2000-02-23  PRIOR PILING DATE: 2000-02-24  PRIOR PILING DATE: 2000-02-24  PRIOR PLING DATE: 2000-02-24  PRIOR PLING DATE: 2000-04-13  PRIOR PLING DATE: 2000-04-13  PRIOR PLING DATE: 2000-04-13	PRIOR FILING DATE: 2000-09-18 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 135 SECTION OF SEQ ID NOS: 2.1	Section   104   104   104   107	98.2%; Score 1368; DB 14; Length 264; larity 99.6%; Pred. No. 1.66-124;	244; COMSCIVACIONE 5 IVGGORAPRSKWPWQVSLRV 20 IVGGORAPRSKWPWQVSLRV	REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP	125 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184

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APPLICANT: Milennium Pharmaceuticals Inc.
APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Alleen
APPLICANT: Weich, Nadine S.
APPLICANT: Kelly, Louise M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
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                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 10/174,364
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/191,947
PRIOR APPLICATION NUMBER: 60/191,947
PRIOR APPLICATION NUMBER: 60/192,665
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-28
PRIOR PLING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: 60/192,664
PRIOR APPLICATION NUMBER: 60/192,664
PRIOR APPLICATION NUMBER: 60/192,664
PRIOR APPLICATION NUMBER: 00/192,064
PRIOR PLING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: 00/192,064
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                                                               APPLICANT: Majumder
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
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                                                                                                                               FILE REFERENCE: 15966-729CIP2CON1
CURRENT APPLICATION NUMBER: US/10/246,583
CURRENT FILING DATE: 2002-12-06
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US20040058862A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 244; Conservative
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Best Local Similarity
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APPLICANT: Wezes, Peter S
APPLICANT: Wezes, Corine A. M.
APPLICANT: Vernet, Corine A. M.
TITING OF INVENTION: NO. US20030148485A1e1 Polypeptides and Amino Acids Encoding Same;
FILE REPERENCE: 15966-729
CURRENT APPLICATION NUMBER: US/09/813,432
CURRENT PLINING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/190,768
PRIOR FILING DATE: 2000-03-20
PRIOR PAPLICATION NUMBER: 60/191,199
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/191,99
PRIOR PETING DATE: 2000-03-28
PRIOR PETING DATE: 2000-03-28
PRIOR PETING DATE: 2000-03-28
PRIOR PELING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGFDVKDLAALRVQL
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US-10-246-583-44
; Sequence 44, Application US/10246583
                                                            Sequence 44, Application US/09813432
Publication No. US20030148485A1
GENERAL INFORMATION:
APPLICANT: Taupier Jr., Raymond J
                                                                                                                                                                                                   Majmuder, Kamud
Spaderna, Steven K
Smithson, Glenda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 275
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US-09-813-432-44
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| TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212, 1TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849, 1TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849, 1TITLE OF INVENTION: 1910, 1021, 837, 1761, 8990 OR 13249 MOLECULES CURRENT APPLICATION NUMBER: US 60/364, 433
| PRIOR TILING DATE: 2003-01-28 | PRIOR APPLICATION NUMBER: US 60/364, 476 | PRIOR PRILING DATE: 2002-02-28 | PRIOR PRILING DATE: 2002-02-28 | PRIOR PRILING DATE: 2002-02-28 | PRIOR PRILING DATE: 2002-03-60/36 | PRIOR PRILING DATE: 2002-03-60/36 | PRIOR PRILING DATE: 2002-04-66 | PRIOR PILING DATE: 2002-06-66 | PRIOR PILING DATE: 2002-66-26 | PRIOR PILING DATE: 2002-66-26 | PRIOR PILING DATE: 2002-66-28 | PRIOR PILING DATE: 2002-06-28 | PRIOR PILING DATE: 2002-06-38 | PRIOR PILING DATE: 2002-06-28 | PRIOR PILING DATE: 2002-06-38 | PRIOR PILING DATE: 2002-07-31 | PRIOR PILING DATE: 2002-06-38 | PRIOR PILING DATE: 2002-07-31 | PRIOR PILING DATE: 2002-06-38 | PRIOR PILING DATE: 2002-06-39 | PRIOR P
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Job time : 941 secs
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US-10-352-684A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 244; Conserval
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us-09-598-982-21.rge
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                              OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                July 22, 2004, 15:27:32
                       Copyright
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; Search time 4800 Seconds (without alignments) 2248.420 Million cell updates/sec 249 US-09-598-982-21 Perfect score: Run on:

1393 1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP 0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Sequence:

6940544

3470272 seqs, 21671516995 residues

Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Command line parameters:

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Database:

GenEmbl:\*

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2: gb\_htg:\*

3: gb\_nt:\*

5: gb\_on:\*

5: gb\_on:\*

6: gb\_on:\*

9b\_pn:\*

9b\_pr:\*

9b\_ro:\*

9b\_sts:\* gb\_vi:\* em\_ba:\* em\_fun:\* em\_hum:\* mu:\* em\_in:\* 71174 71175 71176 7176 7

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em_htgo_mus: *
em_htgo_other: *
em vi:*
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                                             em_htg_mam: *
em_htg_vrt: *
em_sy: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	1393		771	9		47853 Sequence
0 0	38		771	6	AX347869	7869 Sequenc
า 4	1387	9.0	177		AK165112 BX347841	AK165112 Sequence
יני	38		771		BD211490	90
9	1384		771		AX347857	857
7	1384	•	771		AX347859	59 Sequenc
<b>o</b> o (	1382		771		AX347838	Sequenc
10	1379	0.66	771	ρv	AX347855 AX347873	AX347855 Sequence
11	1379		771		AX347875	
12	1374		735		AX347861	1981
13	1374	98.6	771		AX347871	7
14	1369	98.3	735		AX347877	1877
15	1368	98.2	735		AR165109	σ
16 17	1368	98.2	735		AX347843	m t
àΓ	1368	9 0 0 2 0 0 2 0 0	1128		BD21148/	ADOROACI Commondo
19	1368	98.2	1128		HUMTRY2A	ΉΠ
20	1368	98.2	1143		HUMBTRYP	M37488 Human beta-
21	1368	98.2	1145			beta-tr
22	1368	98.2	1194		BC029356	Homo
233	1368	98.0	1235		BC038416	6 Homo
4 C	1365	0. a	735		AX347865 AX347867	AX347865 Sequence
26	1363	97.8	735		AX347834	٠ 🕁
27	1363	97.8	1137		AR080460	AR080460 Sequence
28	1363	97.8	1137		HUMTRY1A	
29	1360	97.6	735		AX347863	AX347863 Sequence
30	1360	97.6	735		AX347881	AX347881 Sequence
32	1350		735		AX347883	AX347883 Sequence
33	1344		1081		AR080462	2
34	1344		1081		AX329646	Sequence 3
35	1344	•	90	9	AX330205	05
36	1344		08	9	AX334644	44
37	1344		08	9	AX375047	47 Sequ
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ALIGNMENTS

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220 999 240

180 546 200

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Maffit, M., Niles, A.L. and Haak-Frendscho, M.
Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same
Patent: WO 0198470-A 36 27-DEC-2001;
PROMEGA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="lekrivgggeaprskwpwqvslrvygpywmhfcggslihpqwvl
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Epvnvsshvhtvtlppaasetpppgmpcwvtgwgdvdndbrlpppfplkqvkpimenh
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GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
667 GGCTGTGCCCAGCCCCAACCGGCCTGGCATCTACACCCCTGTCACCTACTTGGACTGG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 CTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LeuGluLysArgileValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal
                                                                                                                                          547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG
                                                                                                                  AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly
                                                                                                                                                                                           201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu
                                                                                                                                                                                                               IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg
                                                                                   487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCGGT
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 from Patent WO0198470.
AX347869
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/DOCUMENT 1 d="CAD22420.1"
/db_xxef="REMTRERMEL: CAD22420"
/db_xxef="REMTRERMEL: CAD22420"
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NHIODAXYHIGAAYTGDDDVRLYRDDWICAGNNFRDSCQGDSGGFLVCKVNGTWLQAGVV
SWGGGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
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                     01-FEB-2002
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                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                           Maffit,M., Niles,A.L. and Haak-Frendscho,M.
Recombinant proteolytic tryptases, active site mutants thereof,
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Patent: WO 0198470-A 20 27-DEC-2001;
PROMEGA CORPORATION (US)
                                                                                                                                                                                                                                                                                                1. .771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                  AX347853 771 bp
Sequence 20 from Patent WO0198470.
AX347853
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BDZYMAtically-active recombinant human beta-tryptase and method of making same.
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                         667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGG 726
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Maffitt,M.A., Niles,A.L. and Frendscho,M.H.
Enzymatically-active recombinant human beta-tryptase and method of making same
Patent: JP 2002515254-A 4 28-MAY-2002;
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221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp
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PN JP 2002515254-A/4

PP 28-MAY-2002

PF 29-CT-1998 JP 2000549745

PR 15-MAY-1998 US

O9/079970

PI MARK A MAFFITT, ANDREW L NILES, MARY HAAK FRENDSCHO PC

(C12N15/09) CO7XII 640, C12N11/19, C12N9/64, C12P21/08, C12Q1/37//

(C12N9/64, C12R1:645), C12N15/00

CC Strandedness: single;

CC Topology: Linear;

CC Topology: Linear;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                       241 IleHisHisTyrValProLysLysPro 249
                                                                                                                                      ATCCACCACTATGTCCCCAAAAAGCCG 753
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Location/Qualifiers
L. .711
J. .711
J. organism="Homo sapie
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JP 2002515254-A/4.
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Homo sapiens
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BPVKVSSHHHYTLPPASETPPPGMGFWYTGMGDVDNDRRLPPPFPLKQVKVPFMENH
ICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSW
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                                                                                                                                                                                                                                                                                                                      translation="LEKRIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGSTGCAACTGCGGGAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGGAGG 246
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Mismatches:
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/note="unnamed protein product"
/codon_start=1
                                                                                                                                                                                                                               /protein id="CAD22418.1"
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/db_xref="REMTREMBL:CAD22418"
                                                                                                       /mol_type="unassigned DNA'
/db_xref="taxon:9606"
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ICDARKYHLGAYTGDDVRIVRDDMLCAGNITRRDSCQGDAGGFLVCKVNGTWLQAGVVSW
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Recombinant proteolytic tryptases, active site mutants thereof, methods of making same the methods of making same PROMEGA CORPOSATION (US)
                         IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuleuGlu
                                                                             LeuGluGluBroValLysValSerSerHisValHisThrValThrLeuBroProAlaSer
                                                                                            GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp
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AGGGTGCAACTGCGGGAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG
                                                                                                                                                  GAGGGCTCCCACCGCCATTCCTCTGAAGCTGAAGGTCCCCCTAATGGAAAACCAC
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/db_xref="taxon:9606"
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Sequence 24 from Patent W00198470.
AX347857
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/db_xref="G1:18495665"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 26 from Patent WO0198470.
AX347859
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Recombinant proteolytic tryptases, active site mutants thereof, methods of making same
Patent: WO 0194170-A 5.27-DEC-2001;
PROMEGA CORPORATION (US)
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                   Recombinant proteolytic tryptases, active site mutants thereof, methods of making same methods of making same Patent: WO 0199470-A 26 27-DBC-2001; PROMEGA CORPORATION (US)
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Maffit,M., Niles,A.L. and Haak-Frendscho,M.
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	191 CHART GLENT OFFORDER TO LEAD WAS INVALLY STATE TO LIGHT FOR THE STATE STAT	AspAs             	221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240 [	AX347855 771 bp DNA linear PAT 01-FEB-2002 ON Sequence 22 from Patent W00198470. N AX347855 AX347855.1 GI:18495662 Homo sapiens (human)	SM Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  B. 1 S. Maffit,M., Niles,A.L. and Haak-Frendscho,M. Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same	L Patent: WO 0198470-A 22 27-DEC-2001;  PROMEGA CORPORATION (US)  Location/Qualifiers  1. 771  /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	/ Incle="uniqued protein product" / codon start="

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Maffit,M., Niles,A.L. and Haak-Frendscho,M.
Recombinant proteolytic tryptases, active site mutants thereof,
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Patent: WO 0198470-A 40 27-DEC-2001;
PROMEGA CORPORATION (US)
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Momo sapiens
Eukarycia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu
                        221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp
                                                                                                                                                                                                                                                                                                         linear
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/protein_id="cAb22431.1"
/db_xref="G1:1849563"
/db_xref="REMTREMBL:CAD22431"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                             Sequence 42 from Patent WO0198470.
AX347875
AX347875.1 GI:18495682
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KYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGFLVCKVNGTWLQAGVVSWGEGC
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IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu
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/note="unnamed protein product"
/codon_start=="
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/db_xref="GI:18495669"
/db_xref="REMTREMBL:CAD22424"
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

DEFINITION ACCESSION VERSION

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LOCUS

RESULT

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source

FEATURES

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ORIGIN

JOURNAL

PAT 01-FEB-2002

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	and Haah rtic trypte mme 44 27-DEC (US) Lalifiers Homo sapie	/mo.trype="unassigned DNA" /db_xref="taxon:9606" cDS <1>735 /note="unnamed protein product" /codon start=1 /rochoin id="(AD22432.1")	/ DE XTEFE = "A SET	Alignment Scores: 3.12e-120 Length: 735 Pred. No.: 3.12e-120 Matches: 244 Score: 1369.00 Matches: 244 Percent Similarity: 99.59\$ Mismatches: 1 Best Local Similarity: 99.59\$ Mismatches: 1	Gaps: 6 -21 (1-249) x AX347877 (1-735)	Qy 5 11eValGlyGluAlaProArgSerLysTrpFroTrpGlnValSerLeuArgVal 24	Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44	Oy 45 ThralahladaqocysValGlyProAspValLySAspLeuAlahlaLeuArgValGlnLeu 64	Oy 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
TITLE Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same  JOURNAL Patent: WO 0198470-A 38 27-DEC-2001;  PROMEGA CORPORATION (US)  FEATURES  Location/Qualifiers  Location/Qualifier	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Bercent Similarity: 98.80% Conservative: 0 Bert Local Similarity: 98.80% Mismatches: 3 Query Match: 6 Gaps: 0 DB: US-09-598-982-21 (1-249) x AX347871 (1-771)	1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal	Oy 21 Serlentsgrallisty.projyrtrpMeth.sPnecysty.edg.yeztech.enistro 40	Qy         61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80           Db         187 AGGGTGCAACTGCGGGAGCACCTCTACTACTACCAGGCTGCTGCTGGCAGG 246           Qy         81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100           Db         247 ATCATCGTGCACCCAGGTTCTACACCGCCCAGATCGGAGCGCAATCGCCCTGCTGGAG 306	Qy         101 LeuGludluProValLysValSerSerHisValHisThrValThrLeuBroProAlaSer         120           Db         307 CTGGAGGAGGCGGTGAAGGTCTCCAGCCACGTCCACCTGCCCCTGCCCCTGCCCTGCCCTGC         366	Oy 121 GluthrbheproproglyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140	Qy         141 GluargleuProProProPheProLeulysGlnVallysValProIleMetGluAsnHis 160           Db         427 GAGCGCTCCCACCGCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC 486	Qy 161 IleCysAspalaLysTyFHisLeuGlyAlaTyrThrGlyAspAspValArg1leValArg 180	Oy 181 AspAspNetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

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Maffitt,M.A., Niles.A.L. and Haak-Frendscho,M.
Enzymatically-active recombinant human .beta.-tryptase and method of making same
Patent: US 6274366-A 1 14-AUG-2001,
Location/Qualifiers
1. .735
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/mol_type="unassigned DNA"
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13, Appl 19, Appl 5, Appli 5, Appli 5, Appli 2, Appli 9, Appli

Appli Appl:

Sequence 30,

US-08-978-404B-7 US-08-978-404B-4 US-08-978-404B-4 US-08-978-404B-4 US-08-845-998-3 US-09-016-366A-23 US-09-016-366A-13 US-09-016-366A-13 US-09-03-396-5 US-09-03-396-5 US-09-03-396-5 US-09-386-653A-1 US-09-386-642-8 US-09-386-642-8 US-09-386-642-8 US-09-386-642-7 US-09-386-642-7

29, Appli 1, Appli 8, Appli 8, Appli 7, Appli 28, Appl

Sequence

Sequence

262, App 1, Appli 3, Appli

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Sequence Sequence Sequence

US-09-907-794A-256 US-09-905-125A-256 US-09-902-775A-256

34506.073

US-09-023-942A-3

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APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Brzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: MISCONSIN
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09079970A Patent No. 6274366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERENCE/DOCKET NUMBER: 34506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2106
TELEFAX: (608) 831-2106
TELEFAX: (608) 831-2106
SEQUENCE CHARACTERISTICS:
                              1097
1103
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-UOTFWIT=PLO-NOTEMT=PATE -SOON - THR_SOON - THR_MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                        OM protein - nucleic search, using frame_plus_p2n model
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US-09-079-970A-1
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US-09-016-366A-16
US-09-016-366A-16
US-09-016-368-11
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Listing first 45 summaries
                                                                                                         July 22, 2004, 15:38:42
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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61 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 120
667 GGCTGTGCCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG 726
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                                                                                                                                                                                                                                APPLICANT: Maffitt, Mark A.
APPLICANT: Miles, Andrew L.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Braymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                   B: Intellectual Property Department 8000 Excelsior Drive, Suite 401
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                                              241 IleHisHisTyrValProLysLysPro 249
                                                                                      727 Arccaccarrargrececaaaaageeg 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Leone, Joseph T.
REGIGSTRATION NUMBER: 37,170
REPERENCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEPHONE: (608) 831-2106
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      ; Sequence 1, Application US/09079970A; Patent No. 6274366
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1368.00
99.59%
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 735 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.21%
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ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyCysAlaGlnProAsnArgProGly11eTyrThrArgYalThrTyrTyrLeuAspTrp 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCATAATGGAAAACCAC 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 CAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CTCGAGAAAAGAATGGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
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Conservative:
Mismatches:
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1387.00
99.60%
99.60%
                                                                                         DNA (genomic)
    LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: DNA (genomi
                                                                                                          HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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Best Local Similarity:
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LOCATION:
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; LOCATION:
US-09-079-970A-4
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Pred. No.:
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85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluBro 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuileHisProGlnTrpValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 ThralaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 ACCGCAGCGCACTGCGTGGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 CGGGAGCAGCTCTACTACCAGGACCAGCTGCTGCCGGTCAGGATCATCGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 CCACAGTICTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln
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                                                                                                                                                                                                                                                                                                               1128
244
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                            Indels:
Gaps:
                                                                    B0801/7093
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Blizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/POCKET NUMBER: B080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                            3.84e-142
1368.00
99.59%
99.59%
                                                                                                                                         INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
                                                                                                                                                                            LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                             TELEPHONE: 617-720-350
TELEFAX: 617-720-2441
                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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               64
                                                                      ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis
                                                                                                                                                                                                                                                                ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro
                                                                                                 181 CGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC
                                                                                                                                                                                                  105 VallysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro
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                                                                                                                                                                  241 ccacacirciacacceccadaredaacedacaredecerecrecaderedadered
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Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FREESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FLING DATE: January 30, 1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
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ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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569 AAATACCACCTTGGCGCCTACACGGGAGGCGACGTCCGCATCGTCCGTGAGGACATGCTG 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgileValArgAspAspMetLeu 184
                                                                                                                                                                         ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
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                                                                                                   CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
                                                                     85 ProglupheryrThralaGlnIleGlyAlaAspIleAlaLeuCluLeuGluLeuGluEluGluPro
65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis
                                                                                                                                           105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTHARE: FastERE for Windows Version 2.0 SOFTHARE: FastERE for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 18, Application US/09016366A; Patent No. 5955431; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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US-09-016-366A-18
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       149 CCCAACCGGCCTGGCATCTACACCCGTGTCACTTGGACTGGATCCACCACTAT 808
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                                                                                                                                                                                                                 APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINGGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
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Matches:
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                                                                                                                                    RESULT 4
US-08-978-404B-15
Sequence 15, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
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SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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02210-2211
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STRANDEDNESS:
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DB:
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                                                                   Sequence 13, Application US/08978404B

Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
ITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FASISTEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 13:
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1363.00
99.18%
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            807 GTCCCCAAAAGCCG 821
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LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SOFTWARE: FastSEC
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Best Local Similarity:
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                                                    US-08-978-404B-13
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CITY: Bo
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DB:
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                                                                                                                                                                                                                                                                                                                 US-09-598-982-21 (1-249) x US-09-016-366A-18 (1-1137)
                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                Length:
TELECOMMUNICATION INFORMATION:
TELEFRONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
                                                                                                                                                                                                            1.39e-141
1363.00
99.18%
99.18%
                                                         INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValProLysLysPro 249
                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                  US-09-016-366A-18
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DB:
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RESULT 8
US-08-978-404B-17
; Sequence 17, Application US/08978404B
              LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
 SEOUENCE CHARACTERISTICS:
                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                          MOLECULE TYPE:
                                                                                             US-09-016-366A-22
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                                                                                                                                                                                                                                   LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu 184
                                              ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
GTGAACGTCTCCAGCCACGTCCACACGTCACCCTGCCCCTGCCTCCAGAGACCTTCCCC
                                                                                                                                                                                                                                                                                                                         TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGC
                                                                                                             ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro
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APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOSS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09016366A Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,63
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ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5955431
GENERAL INFORMATION:
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STREET: 600
CITY: Bostc
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1081
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                                        Conservative:
Mismatches:
Indels:
                                                                                                                                      US-09-598-982-21 (1-249) x US-09-016-366A-22 (1-1081)
      Length:
Matches:
    1.65e-139
1344.00
98.37%
98.37%
96.48%
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125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspAspGluArgLeuPro 144
            368 GTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC 427
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APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUMTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston
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REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09016366A Patent No. 5955431 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
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Patent No. 5969782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIRRINGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                             COMPUTEK: IDEN COMPUTEM:
OPERATING SYSTEM: DOS
SOFTWARE: FRRESEQ for Windows Version 2.0
SOFTWARE: PRESESCO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION DATA:
APPLICATION NUMBER: 00/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 80801/7090
TELECOMMINICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-598-982-21 (1-249) x US-08-978-404B-17 (1-1081)
                                                                                                                                ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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98.378
98.378
96.48%
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TYPE: nucleic acid
STRANDEDNESS: single
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02210-2211
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Best Local Similarity:
                                                                                                                                                                          Boston
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                                                                                                                                                                        CITY: B
STATE:
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CORRESPONDENCE ADDRESS:
                                                                      COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
NUMBER OF SEQUENCES:
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Best Local Similarity:
                                                Boston
                                                                                                             MEDIUM TYPE:
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TOPOLOGY:
US-08-978-404B-11
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                                                                            Conservative:
                                                                                                                                        US-09-598-982-21 (1-249) x US-09-016-366A-16 (1-1154)
                                                                                       Mismatches:
Indels:
                                                  Length:
Matches:
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Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROI
TITLE OF INVENTION: FIBRINGEN
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                                                  1.05e-131
1274.00
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                                                                           Percent Similarity:
Best Local Similarity:
   MOLECULE TYPE:
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US-08-978-404B-11
      ; MOLECULE TYPE
US-09-016-366A-16
                                        Alignment Scores:
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Mismatches:
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                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
E: Wolf, Greenfield & Sacks, 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                   E: Diskette
IBM Compatible
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94.698
92.248
91.468
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LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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             Percent Similarity:
Best Local Similarity:
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        ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla
                                  528 CCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA
                                                                 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLeu
                                                                                     588 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCATCCGTGACGACGACGACGTG
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENTING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERNCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09016366A
Patent No. 5955431
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APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 02210-2211
COMPUTER READABLE FORM:
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                                                                                                                                                                                                    127 ATCGTGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGATTT
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                                                                                                                                                                                                                                             25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu
                                                                                                                                                                                                                                                                                                                           45 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667 IGIGCIGGAAATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGGGGCCACTGGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
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               Conservative:
Mismatches:
                                                                                                                      US-09-598-982-21 (1-249) x US-09-016-366A-14 (1-1108)
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; Patent No. 5968782;
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CI
TITLE OF INVENTION: FIBRINOGEN
TITLE OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
  Matches:
                                                              Indels:
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127 AAAGTGAAGGGTACCTGGCTGCAGGCAGGAGTGGTCAGCTGGGGGTGAGGGCTGAGGGCTGAGGCCACAGA 786
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                                                                                                                                           607 AAGTACCACACTGGCCTCTACACGGGAGATGATTTTCCCATTGTCCATGATGGCATGCTG
                                                                                                           185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
                                                                                                                                                                                                                      205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln
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188
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TITLE OF INVENTION: MASI CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks,
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.31e-109
1075.00
84.77$
77.37$
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STRANDEDNESS: single
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
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847 GTCCCTGAG 855
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Best Local Similarity:
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Pred. No.:
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US-08-978-404B-7
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Mismatches:
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                                                                                                                                                SOFTWARE: FASTEM: DOS SOFTWARE: FASTED for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,404B FLING DATE: 25-NOV-97 CLASSIFTCATTON TOWN PATER TOWN STREET TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET UNMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                 E: Diskette
IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 1108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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78.19%
78.32%
                            COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
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US-08-978-404B-20
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version
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1054.00
83.54%
76.54%
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                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        75.66%
                                                                                                                                                                                                                     nucleic acid
EDNESS: single
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US-08-978-404B-1
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   5 lleValGlyGlyGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal
                                                                                            ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu
                                                                     65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArglleIleValHis
                                                                                                                                                        ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluGluPro
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Patent No. 5968782
GENERAL INFORMATION:
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINGGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
MUMBERSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Boston
CITY: Boston
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MEDIUM TYPE: Diskette
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Mismatches:
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Matches:
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CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRICK APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Blizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOME: 617-720-3500
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173 AAAIICAGCIICIGGAIGCAIITICIGIGGCGCCICCCICATICACCCACAGIGGGIGCIC
                                                                                      65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis
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Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02210-2211

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETSO
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION 1435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTOMNEY/AGRAY INPORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
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Matches:
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600 Atlantic Avenue
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
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LENGTH: 1097 base pairs
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INFORMATION FOR SEQ ID NO:
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EDNESS: single
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Best Local Similarity:
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CITY: Boston
STATE: MA
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Title:

Run on:

Sequence:

Scoring table:

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DNA construct for producing enzymatically-inactive proteolytic tryptase,
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P-PSDB; AAU12009.
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22, 2004, 15:26:22; Search time 474 Seconds (without alignments) 2231.648 Million cell updates/sec
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Aas20765 |
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                 OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                            3373863 seqs, 2124099041 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database :

1388 1387 1387 1384 1384 1382

0 m 4 m 9 r 0

Result No.

comprises DNA sequence encoding proteolytic tryptase having an active site mutation.

Claim 7; Page 83-84; 126pp; English

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a none secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its crombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. site mutants

Sequence 771 BP; 147 A; 256 C; 244 G; 124 T; 0 U; 0 Other;

IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180 546 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200 366 140 246 GluargleuProProPheProLeuLysGlnValLysValProlleMetGluAsnHis 160 486 126 186 IlelleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100 9 80 99 40 GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC CIGGAGGAGCCGGIGAAGGICTICCAGCCACGICCACACACACACCCTGCCCCGCCTGCCTCA SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro GInTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer GluthrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp LeuGluLysArgileValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 67 Agecheagadrecaeddececaraerdeardeartearrecaedddaecreereareed ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 187 AggengcaAcnecegeaacacacarcriacnacaggaccagcrecrecegeaacaag gadacchreceeceeeeaheeceneereereereereereereeeeeeeeeeee 771 249 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-771)US-09-598-982-21 (1-249) x AAS20775 2.04e-121 1393.00 100.00% 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: 247 161 61 81 101 307 121 367 141 427 21 41 7 Query Match: DB: g g ð 원 a  $\stackrel{>}{\circ}$ a ò q  $\delta$ g ð à 셤 à ð δ

771

Length:

6.02e-121

Alignment Scores: Pred. No.:

The present invention relates to recombinant human proteclytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteclytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The active site mutants of proteolyfic tryptase provide a tool to investigate the structural and functional properties of the protease and its the structural and functional properties of the protease and its crecombinant proteolyfic tryptase produced are useful as an antigen to generate anti-human tryptase antibitors, antagonists, agonists, etc.

ASSOUTS-AASSO790 encode for recombinant human beta-II tryptase active 240 726 999 DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active 547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 201 ProLeuvalCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu GlyCysalaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp Human; proteclytic tryptase; protease; recombinant beta-II tryptase; DNA encoding human beta-II tryptase active site mutant H44A #3 G; 124 T; 0 U; 0 Other; 249 Haak-Frendscho M; Claim 7; Page 104-105; 126pp; English 241 IleHisHisTyrValProLysLysPro Sequence 771 BP; 147 A; 257 C; 243 BP 20-JUN-2001; 2001WO-US019681. 21-JUN-2000; 2000US-00598982 AAS20783 standard; DNA; 771 09-APR-2002 (first entry) Maffit M, Niles AL, (PROM-) PROMEGA CORP WPI; 2002-114578/15. enzyme; mutant; ds. P-PSDB; AAU12017 WO200198470-A2. site mutation. site mutants sapiens 27-DEC-2001. Synthetic AAS20783; 221 RESULT 2 AAS20783 à 셤

us-09-598-982-21.rng

Haak-Frendscho M;

Maffitt MA, Niles AL, (PROM-) PROMEGA CORP

98WO-US022994.

29-OCT-1998;

25-NOV-1999

Homo sapiens

WO9960139-A1

98US-00079970

15-MAY-1998;

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This sequence encodes the human beta-tryptase. The invention relates to a signal sequence which is linked to a sequence encoding human beta-ctryptase. The DNA construct is useful for transforming human beta-ctryptase. The DNA construct is useful for transforming host cells to express, post translationally process and secrete enzymatically active human tryptase. The method is useful for the production of large amounts of tryptase with defined specifications. The transformant is useful for crystallographic studies, combinatorial library screens and X ray crystallographic studies. The tryptase produced allows for the crystallographic studies. The tryptase produced allows for the or crystallographic studies. The tryptase antibodies in various animals, can antigen to generate antihuman tryptase antibodies in various animals, can clevelopment of tryptase agonists antigonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists of post-expression or post-purification modifications or manipulations to initiate tryptase activity and it has enzymatic activity which compares construction tryptase facilitates the large scale screening of combinatorial dransace for tryptase inhibitors as potential therapeutics and advances the understanding of the biological significance of tryptase in mark rell mark re
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Beta-tryptase, human, DNA expression construct, protein production, combinatorial library screening; X ray crystallography; antigen;

antibody generation; ss.

Human beta-tryptase coding sequence.

(first entry)

18-FEB-2000

AAZ40175;

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                                                                                          GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
                                                                                                                             GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
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                                                       LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
                                                                                                           187 AGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGG 246
                                                                                                                                                                                                                    GACGACATGCTGTGTGTGCCGGGGAACACCCGGAGGGGACTCATGCCAGGGCGACTCCGGAGGG
                            CTGGAGGAGCCGGTGAAGGTCTCCAGCCACACGGTCACCGTCACCCTGCCCCTGCCTCA
                                                                                                                                                                  IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg
                                                                                                                                                                                                                                        ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu
                                                                                                                                                                           Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
enzyme; gene; mutant; ds.
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/note= "This sequence lacks a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding recombinant human beta-II tryptase.
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                                                                                                                                                                                                                                                                                                                                   Arccaccacrargrececaaaaageeg 753
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                                                                                                                                                                                                                                                                                                                                                                       AAS20765 standard; DNA; 771 BP
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the cative site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its crombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. The present sequence encodes for recombinant human beta-II tryptase
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                                                                       DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                               Claim 43; Page 75-77; 126pp; English.
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1387.00
99.60%
99.50%
WPI; 2002-114578/15.
P-PSDB; AAU12007.
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Best Local Similarity:
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                                                                 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
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              GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG
                                 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu
                                              AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly
                                                                                                                                                                                                                          Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
                                                                                                                                                                                                          DNA encoding human beta-II tryptase active site mutant S194A #2.
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                                                                                                             Haak-Frendscho M;
                                                                                                    IleHisHisTyrValProLysLysPro
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The present invention relates to recombinant human proteclytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteclytic cryptase that lacks enzymatic activity due to the active site mutation, (the construct drives expression of a mature proteclytic tryptase that lacks enzymatic activity due to the active site mutants of proteclytic tryptase provide a tool to investigate active site mutants of proteclytic tryptase provide a tool to investigate the structural and functional properties of the protease and its encompainant proteclytic tryptase produced are useful as an antigen to generate anti-human tryptase antiholdies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, accive active active Claim 7; Page 91-92; 126pp; English.

Sequence 771 BP; 152 A; 255 C; 241 G; 123 T; 0 U; 0 Other;

site mutants

67 AGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCCC 126 246 100 120 366 140 160 180 546 200 306 426 486 909 220 999 726 CAGTGGTGCTGACCGCAGGGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTC 186 99 40 09 80 LeuGluLysArgIleValGlyGlyGluAlaProArgSerLysTrpProTrpGlnVal CTCGAGAAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCTGGCAAGTG SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeulleHisPro ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspAspAsp GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArglleValArg GInTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer ATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGT AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly GACGACATGCTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAAGGAGACGCCGGGA ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 367 GAGACCTICCCCCGGGGAIGCCGIGCTGGGICACTGGCTGGGGCGAIGTGGACAAIGAI 427 GAGGGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC DNA encoding human beta-II tryptase active site mutant S194A #1. 771 247 1 1 0 Length: Matches: Conservative: Mismatches: Indels: 241 IleHisHisTyrValProLysLysPro 249 Gaps: US-09-598-982-21 (1-249) x AAS20778 (1-771) 1,43e-120 1384.00 99.60% 99.20% AAS20777 standard; DNA; 771 (first entry) Percent Similarity: Best Local Similarity: Alignment Scores: 09-APR-2002 41 187 101 121 141 487 181 201 Query Match: Pred. No.: RESULT 6 AAS20777 à g g g g g ò à g à d à 셤 ð ò ò à Dp à 엄 à g ð 셤 ð 셤 

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81 IlelleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
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                                                                                                                                                                                                                                                                                           DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
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    Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
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1384.00
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                                                                                                                                                                      21-JUN-2000; 2000US-00598982
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                                                                                                                                                                                                  (PROM-) PROMEGA CORP
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                 enzyme; mutant; ds
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                                                            Synthetic.
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247 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG
                                                               101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer
                                                                                                                                                     121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp
                                                                                                                                                                                              367 GAGACCTTCCCCCCCGGGGATGCCGTGCTGGGTCACTGGGGCGATGTGGATGATGAT
                                                                                                                                                                                                                                       GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis
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/note= "This sequence lacks a start codon"
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P-PSDB; AAU12006.
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us-09-598-982-21.rng

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing actives in method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic cryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its crombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc.

The present sequence encodes for human beta-I tryptase comprises DNA sequence encoding proteolytic tryptase having an active Disclosure; Page 72-74; 126pp; English 

Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: Indels: 2.2e-120 1382.00 99.20% 99.20% Best Local Similarity: Percent Similarity: Aliqnment Scores: Query Match:

246 | IlelleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100 ATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120 GluIhrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspAsp 140 426 486 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180 546 547 GACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGG 606 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeulleHisPro 40 9 CTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTG 66 80 1 LeuGluLysArglleValGlyGlyGlyGluAlaProArgSerIysTrpProTrpGlnVal ArgvalG1nLeuArgG1uG1nHisLeuTyrTyrG1nAspG1nLeuLeuProValSerArg CTGGAGGGGGGGGAACGTCTCCAGCCACGTCCACGGTCACCCTGCCCTGCCTCA GluArgLeuProProProPheProLeuLysGlnValLysValProlleMetGluAsnHis GAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCAC AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu ATTIGIGACGCAAAATACCACCTTGGCGCCTACACGGGAGGACGACGTCCGCATCGTCCGT US-09-598-982-21 (1-249) x AAS20763 (1-771) 127 307 21 41 61 187 247 121 367 141 427 161 181 81 101 ð 셤 à g ò d g à q à d  $\delta$ g à ð à ð

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Sequence 771

Alignment Scores: Pred. No.:

771

4.21e-120 1379.00

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence which is operably linked to a bNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the cative site mutanison, in hosts transformed to contain the construct). The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its carymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for 240 compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II tryptase active ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu GlyCysAlaGlnProAsnArgProGly1leTyrThrArgValThrTyrTyrLeuAspTrp 667 GGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGG Human; proteolytic tryptase; protease; recombinant beta-II tryptase; DNA encoding human beta-II tryptase active site mutant S194A #6. DNA construct for producing enzymatically-inactive proteolytic comprises DNA sequence encoding proteolytic tryptase having an 241 IleHisHisTyrValProLysLysPro 249 727 Arccaccacrargrececaaaaacce 753 Haak-Frendscho M; Claim 7; Page 113-114; 126pp; English. 20-JUN-2001; 2001WO-US019681. 21-JUN-2000; 2000US-00598982. AAS20786 standard; DNA; 771 09-APR-2002 (first entry) Maffit M, Niles AL, (PROM-) PROMEGA CORP WPI; 2002-114578/15 enzyme; mutant; ds P-PSDB; AAU12020 WO200198470-A2. site mutation. Homo sapiens site mutants 27-DEC-2001 201 AAS20786; Synthetic 221 RESULT 8 Dp ð 셤

Haak-Frendscho M;

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20-JUN-2001; 2001WO-US019681
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                                                                                          (PROM-) PROMEGA CORP
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P-PSDB; AAU12019.
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enzyme; mutant; ds.
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence which is operably linked to a non-secretion signal sequence tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the cative site mutation, in hosts transformed to contain the construct). The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its the structural and functional properties of the protease and its creombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antegonists, agonists, etc.
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DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
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Mismatches:
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Best Local Similarity:
                                                                                   site mutation.
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186

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81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100 

247

Homo sapiens

61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg

127 cadrodorióchdaccochácdeachdeadaccódacarcaaddarchadcaccaccarc

which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to compounds which act as tryptase antibodies and indrug screening for compounds which act as tryptase inhibitors, antagonists, agonists, agonists, assetive

U; 0 Other;

BP; 149 A; 256 C; 242 G; 124 T; 0

Sequence 771 site mutants

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                      307 CTGGAGGAGCCGGTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCTGCCTCA
                                               GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp
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LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer
                                                                                               GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis
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enzyme; mutant; ds.
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The present invention relates to recombinant human proteolytic tryptases, extive site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence

Claim 7; Page 86-87; 126pp; English.

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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comparising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic which is operably linked to a DNA sequence encoding a proteolytic cryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its chost active site activity, and for modelling studies. The enzymatically-active, compounds which act as tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, active
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                                                                                                                                                                                                                          Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
                                                                                                                                                                                        DNA encoding human beta-II tryptase active site mutant H44A #2
Haak-Frendscho M;
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AAS20779
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5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTxpGlnValSerLeuArgVal 24
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US-09-598-982-21 (1-249) x AAS20779 (1-735)

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241 CCACAGTTCTACACCGCCCAGATCGGAGGACATCGCCCTGCTGGAGCTGGAGGAGCCG 300
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                                              HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu
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enzyme; mutant; ds.
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence tryptase with an active of a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its encompainant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc.

ASC20775-AAS207790 encode for recombinant human beta-II tryptase active
                                                                                                                                                                                                   DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
                                                                                        Haak-Frendscho M;
                                                                                                                                                                                                                                                                                             Claim 7; Page 107-109; 126pp; English.
21-JUN-2000; 2000US-00598982.
                                                                                   Maffit M, Niles AL,
                                                                                                                                WPI; 2002-114578/15.
                                                                                                                                                        P-PSDB; AAU12018
                                                                                                                                                                                                                                                     site mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site mutants
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Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.24e-119 1374.00 98.80% 98.80% 98.80% Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

7711 US-09-598-982-21 (1-249) x AAS20784

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic a mature proteolytic tryptase site mutation (the construct drives expression of active site mutation (the construct drives expression of active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active,

Example 1c; Page 115-117; 126pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.
GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis
                                 GAGGGCTCCCACCGCCATTTCCTCTGAGCAGGTGAAGGTCCCCATAATGGAAAACCAC
                                                                                                              | IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArglleValArg
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                                                                                                                                                                                                                                                                                                                                                    ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human beta-II tryptase active site mutant H44A #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IleHisHisTyrValProLysLysPro 249
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P-PSDB; AAU12021.
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recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug soreening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS207790 encode for recombinant human beta-II tryptase active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis
                                                                                                                                                                                                                                                                                             ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAACTGGCCCTGGCAGGTGAGCTCAAGAGTC
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                                                                                           Sequence 735 BP; 139 A; 246 C; 230 G; 120 T; 0 U; 0 Other;
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1369.00
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AAZ40172 standard; DNA; 735

AAZ40172 ID AAZ4

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This sequence encodes the human beta-tryptase. The invention relates to a paralles signal sequence which is linked to a sequence encoding human beta-tryptase. The DNA construct is useful for transforming human beta-tryptase. The DNA construct is useful for transforming host cells to express, post translationally process and secrete enzymatically active human tryptase. The method is useful for the production of large amounts of tryptase with defined specifications. The transformant is useful for pharmacological studies, combinatorial library screens and X ray crystallographic studies. The tryptase produced allows for the development of tryptase agonists and/or antagonists, is useful as an antiquent to generate antihuman tryptase antibodies in various animals, can be used in screening for compounds which act as tryptase inhibitors, antagonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists etc. may be useful as therapeutics. The tryptase does not require any post-expression or post-purification modifications on manipulations to post-expression or post-purification modifications on manipulations to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiate tryptase activity and it has enzymatic activity which compares favourably with cadaveric tryptase. The availability of enzymatically active tryptase facilitates the large scale screening of combinatorial libraries for specific tryptase inhibitors as potential therapeutics and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           advances the understanding of the biological significance of tryptase in mast cell mediated diseases. The tryptase can be used to detect low
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                                                                                                                     Beta-tryptase; human; DNA expression construct; protein production; combinatorial library screening; X ray crystallography; antigen; antibody generation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA expression construct for production of enzymatically active
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                                                                                           Human beta-tryptase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 40-41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant human beta-tryptase.
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Best Local Similarity:
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                                                     18-FEB-2000
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                                                                                                                                                                                                                                                         CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACATGATGAGCGCCTCCCA 420
                                                                                                                                                                                                                                                                                ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
                                                                                                                                                                                                                                                                                                                              LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArglleValArgAspAspMetLeu 184
                                                                                                                                                                                                                                                                                                                                                                                                  TGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGTGC 600
                    CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCTCATCCACCCCCAGTGGGTGCTG 120
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'product= "Recombinant mature beta-II tryptase"
'note= "This sequence lacks both start and stop codons"
                                                                                                                                                                                                  GTGAAGGTCTCCAGCCACGTCCACACGTCACCCTGCCCCCTGCCTCAGAGACCTTCCCC
                                                                                                                                                                                                                                 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro
                                                                                                                                                                                                                                                                                                   CCGCCATTTCCTCTGAAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                        LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln
                                                                   121 ACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG
                                                                                         ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis
                                                                                                                                       ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro
                                                                                                                                                                                                                                                                                                                                                                            CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu
                                             ThralaalaalaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
enzyme; gene; mutant; ds.
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The present invention relates to recombinant human proteclytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence which is operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteclytic tryptase with an active site mutation (the construct drives expression of a mature proteclytic tryptase that lacks enzymatic activity due to the active site mutants of proteclyfic tryptase provide a tool to investigate the structural and functional properties of the protease and its crombinant proteclytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antegonists, agonists, etc. The present sequence encodes for recombinant human mature beta-II
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                                                                                                                                                                                                                                                                                                                                                                                       DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 78-79; 126pp; English
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                                                                     21-JUN-2000; 2000US-00598982
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P-PSDB; AAU12008.
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ProGlyMetProcysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
                       ProProPheProLeuLysGlnValLysValProlleWetGluAsnHisIleCysAspAla 164
                                                                    LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
                                                                                                                   ProAshArgProGly11eTyrThrArgValThrTyrTyrLeuAspTrp11eHisHisTyr 244
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Title: Perfect score: Sequence:

1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP BLOSUM62
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Description

Sequence 11, Appl Sequence 11, Appl Sequence 1, Appl Sequence 2, Appli Sequence 15, Appl Sequence 21, Appl Sequence 29, Appl 30, Appl 20, Appl 1, Appli 1, Appli 221, App 21, Appl 21, Appl 21, Appl 3, Appli 22, Appli 1, Appli Sequence 2126, A Sequence 2126, A Sequence 680 Sequence 34, A Sequence 36, A Sequence 36, A Sequence 21, A Sequence 4 Sequence 2 Sequence Sequence Sequence 1 Sequence 6 US-10-352-684A-47
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7 US-09-954-456-2126
6 US-09-954-456-2126
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1 US-10-14-493-221
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# ALIGNMENTS

APPLICANT: Millennium Pharmaceuticals Inc. APPLICANT: Carroll, Joseph M. Sequence 47, Application US/10352684A Publication No. US20030215452A1 GENERAL INFORMATION: RESULT 1 US-10-352-684A-47

APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 1871, 1361, 1847, 1849,
TITLE OF INVENTION: 15402, 340, 10217, 837, 1410, 137, 1871, 13051, 1847, 1849,
TITLE OF INVENTION: 15402, 340, 10217, 837, 1410, 137, 13914, 1849,
TITLE OF INVENTION UNMERR: US/10/352,684A
CURRENT APPLICATION NUMBER: US 60/354,333
PRIOR APPLICATION NUMBER: US 60/354,333
PRIOR APPLICATION NUMBER: US 60/364,476
PRIOR APPLICATION NUMBER: US 60/366,258
PRIOR APPLICATION NUMBER: US 60/364,476

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756 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTTGGACTGGATCCACTAT 815
185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
                 205 LysvalasnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/287,226 CURRENT FILING DATE: 2002-11-04
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PRIOR PILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-0134,421
PRIOR PELING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/360,148
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR PILING DATE: 2002-02-7
PRIOR PILING DATE: 2002-03-13
PRIOR FILING DATE: 2002-03-13
PRIOR FILING DATE: 2002-08-20
PRIOR PILING DATE: 2003-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, Jr., Raymond J.,
Vernet, Corine A.M.,
                                                                                                                                                                                                                                                                                                                                ; Sequence 93, Application US/10287226; Publication No. US20040086875A1; GENERAL INFORMATION:
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Patturajan, Meera,
Rastelli, Luca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
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Chant, John S.,
Chaudhuri, Amitabha,
DiPippo, Vincent A.,
Edinger, Shlomit R.,
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Millet, Isabelle,
Ooi, Chean Eng,
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APPLICANT: Alsobrook, John P.,
BERGHS, Constance,
APPLICANT: Boldog, Ference,
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Gangolli, Esha A.
Gorman, Linda,
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Ji, Weizhen,
Kekuda, Ramesh,
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Conservative:
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PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/375,626
PRIOR FILING DATE: 2002-04-26
PRIOR PLING DATE: 2002-06-6
PRIOR APPLICATION NUMBER: US 60/386,494
PRIOR PILING DATE: 2002-06-6
PRIOR PILING DATE: 2002-06-24
PRIOR FILING DATE: 2002-06-24
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-31
PRIOR FILING DATE: 2002-08-13
Remaining FILING DATE: 2002-08-13
SCOTUMARE: FastSEQ for Windows Version 4.0
SEQINOMINE STORM NOS: 62
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Gaps:
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1368.00
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ORGANISM: Homo Sapiens
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Best Local Similarity:
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US-10-352-684A-47
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                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1143
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 104
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    See File Wrapper or PALM.

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Mismatches:
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PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,409
PRIOR FILING DATE: 2002-02-04
PRIOR FILING DATE: 2002-03-03
PRIOR FILING DATE: 2002-03-13
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-20
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ORGANISM: Homo sapiens
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Best Local Similarity:
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; NAME/KEY: CDS
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US-10-287-226-93
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CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACCAT 817
                                                  225 ProdsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
698 AAGGIGAAIGGCACCIGGCIGCAGGCGGGGCGIGGICAGCIGGGGCGAGGGCIGIGCCCAG 757
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CURRENT APPLICATION NUMBER: 08/10/287,226
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 60/334,421
PRIOR APPLICATION NUMBER: 60/354,392
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/354,000
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-07
PRIOR PILING DATE: 2002-03-13
PRIOR PLING DATE: 2002-03-13
PRIOR PLING DATE: 2002-03-03
PRIOR PLING DATE: 2002-03-03
PRIOR PLING DATE: 2002-03-03
PRIOR PLING DATE: 2001-11-30
PRIOR PLING DATE: 2001-11-30
PRIOR PLING DATE: 2001-11-30
PRIOR PLING DATE: 2002-03-13
PRIOR PLING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/354,409
PRIOR PLING DATE: 2002-03-13
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Spaderna, Steven K.,
Spytek, Kimberley A.,
Taupier, T., Raymond J
Vernet, Corine A.M.,
                                                                                                                                                                                                                                                                                                                                       Sequence 91, Application US/10287226 Publication No. US20040086875A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess, Catherine E.,
Chant, John S.,
Chaudhuri, Amitabha,
DiPippo, Vincent A.,
Edinger, Shlomit R.,
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Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles B.,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Ference,
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Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
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Rothenberg, Mark E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Khramtsov, Nikolai,
                                                                                                                                                                   245 ValProLysLysPro 249
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                                                                                                                                                                                                                            GTCCCCAAAAAGCCCG 832
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Ort, Tatiana,
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151 CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGGGATGCCGTGCTGGCTGGCTGGGCGATGTGGATGATGATGATGACCCCCCC 510
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PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/331,641
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 673
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 91
LENGTH: 828
TYPE: DNA
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1363.00
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US-10-287-226-91
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Best Local Similarity:
Query Match:
DB:
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Mismatches:
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Matches:
                                             US-09-954-456-2126
; Sequence 2126, Application US/09954456
; Patent No. US20020115057A1
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; ORGANISM: Homo sapiens
US-09-954-456-2126
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Best Local Similarity:
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Sequence 427, Application US/09873319A

Sequence 427, Application US/09873319A

Publication No. US20030134324A1

GENERAL IRPORMATION:

APPLICANT: Munger, William E.

APPLICANT: Mander, William E.

APPLICANT: Getzenberg, Robert H.

APPLICANT: Getzenberg, Robert H.

APPLICANT: Getzenberg, Robert H.

APPLICANT: Mander, Jun

TITLE OF INVENTION: Hyperplacia Using Gene Expression Profiles

TITLE OF INVENTION: Hyperplacia Using Gene Expression Profiles

FILE REFERENCE: 44921-5029-08

CURRENT APPLICATION NUMBER: US/09/873,319A

CURRENT FILING DATE: 2001-06-05

EARLIER APPLICANTON NUMBER: US 60/223,323

EARLIER PILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 755

SOFFWARE: Patentin Ver. 2.1
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128 CGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 187
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US-09-873-319-427
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
TITLE OF INVENTION: Gene Expression Profiles
TITLE OF INVENTION: Gene Expression Profiles
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-529-019-09-24
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 680
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                          GTGAAGGTCTCCAGCCACGTCACACGGTCACCTGCCCCTGCCTCAGAGACCTTCCCC 427
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Indels:
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us-09-598-982-21.rnpb

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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
FRIOR APPLICATION NUMBER: U.S. 60/236,891
FRIOR APPLICATION NUMBER: U.S. 60/236,892
FRIOR APPLICATION NUMBER: U.S. 60/244,867
FRIOR APPLICATION NUMBER: U.S. 60/244,867
FRIOR FILING DATE: 2000-01-01
FRIOR FILING DATE: 2000-11-01
FRIOR FILING DATE: 2000-11-01
FRIOR FILING DATE: 2000-11-01
FRIOR FILING DATE: 2000-11-01
FRIOR APPLICATION NUMBER: U.S. 60/245,084
FRIOR FILING DATE: 2000-11-01
FRIOR APPLICATION NUMBER: U.S. 60/245,084
FRIOR PLING DATE: 2000-11-01
FRIOR APPLICATION NUMBER: U.S. 60/245,084
FRIOR PLING DATE: 2000-11-01
FRIOR APPLICATION NUMBER: U.S. 60/245,084
FRIOR FILING DATE: 2000-11-01
FRIOR APPLICATION NUMBER: U.S. 60/245,084
FRIOR FILING DATE: 2000-11-01
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ORGANISM: Homo sapiens
US-09-873-367C-155
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Best Local Similarity:
Query Match:
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Matches:
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Indels:
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APPLICANT: Young, Paul
APPLICANT: Bndress, Gregory
APPLICANT: Augustus, Meena
APPLICANT: Augustus, Meena
APPLICANT: Enner, Reinhard
APPLICANT: Carter, Kenneth
                   1.94e-155
1344.00
98.37%
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US-09-873-367C-155
     Alignment Scores:
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ProAsnArgProGly11eTyrThrArgValThrTyrTyrLeuAspTrp11eHisHisTyr 244
ProProPheProLeuLysGlnValLysValProlleMetGluAsnHisIleCysAspAla 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668 AAGGTGAATGGCACCTGGCTGCAGGCGGGGGTGGTCAGCTGGGGGCGAGGGCTGTGCCCAG 727
                                                                                  ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro
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APPLICANT: BELEGEANE, Angelo M.; LAL, Preeti G.
APPLICANT: HARALIA, April J.A.; PATRESSON, Chandra
APPLICANT: HARALIA, April J.A.; PATRESSON, Chandra
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda; ELLIJOTT, VICKI S.
APPLICANT: WGUYEN, Danniel B.; GANDHI, Ameena R.
APPLICANT: POLICKY, Jennifer L.; LU, Dyung Aina M.
APPLICANT: REDDY, ROOPE M.; YUE, Henry
APPLICANT: REDDY, ROOPE M.; YUE, Henry
TITLE OF INVENTION: PROFIERSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/275,505
CURRENT APPLICATION NUMBER: US/10/275,505
CURRENT FILING DATE: 2002-11-04
FRIOR APPLICATION NUMBER: PCT/US01/14651
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-05-17
PRIOR FILING DATE: 2000-05-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/10275505; Publication No. US20040081961A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Soppet, Daniel
APPLICANT: Borey, Paul
APPLICANT: Borey, Meena
APPLICANT: Reinhard
APPLICANT: Carter, Reinhard
APPLICANTON NUMBER: US,00/873,367C
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR PILING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SEQ ID NOS: 1067
ANNINGEN OF ELENGTHS: 1081
                                                      ProAsnArgProGly11eTyrThrArgValThrTyrTyrLeuAspTrp11eHisHisTyr 244
                                                                                     728 CCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAGGACTGGATCCACCACTAT 787
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  AAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGGCGAGGGCTGTGCCCCAG 727
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Mismatches:
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Publication No. US20030165839A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
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1344.00
98.37%
98.37%
96.48%
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APPLICANT: SPYTEK, KINDERIEW, A.,
APPLICANT: Taupier, Tir, Raymond J.,
APPLICANT: Taupier, Corine A.M.,
APPLICANT: Zhong, Mei
TTILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-480C
CURRENT PILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: 06/354,322
PRIOR PILING DATE: 2002-01-030
PRIOR PILING DATE: 2002-02-07
PRIOR PILING DATE: 2002-02-07
PRIOR PELING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/360,148
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR PELING DATE: 2002-02-07
PRIOR PELING DATE: 2002-08-03
PRIOR PELING DATE: 2002-08-03
PRIOR PELING DATE: 2002-08-03
PRIOR PELING DATE: 2002-08-04
PRIOR PELING DATE: 2001-11-30
PRIOR PELING DATE: 2001-11-30
PRIOR PELING DATE: 2001-01-130
PRIOR PELING DATE: 2001-01-130
PRIOR APPLICATION NUMBER: 60/354,409
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/331,641
PRIOR APPLICATION NUMBER: 60/334,027
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PRIOR APPLICATION NUMBER: 60/334,027
PRIOR APPLICATION NUMBER: 60/334
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Matches:
Conservative:
Burgess, Catherine E.,
Chant, John S.,
Chaudhuri, Amitabha,
DiPippo, Vincent A.,
Edinger, Shlomit R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ooi, Chean Eng,
Ort, Tatiana,
Padigaru, Muralidhara,
                                                                                                                                                                                                                                                                                                 Li, Li,
Malyankar, Uriel M.,
MacDougall, John R.,
Mazes, Peter S.
Miller, Charles E.,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patturajan, Meera,
Rastelli, Luca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spytek, Kimberley A
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1323.00
97.14%
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Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
                                                                                                                                                                                                                                                                            Khramtsov, Nikolai,
                                                                                                                                                                                                                             Ji, Weizhen,
Kekuda, Ramesh,
                                                                                                                    Eisen, Andrew,
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ORGANISM: Homo sapiens
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US-10-287-226-89
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Matches:
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Indels:
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GENERAL INFORMATION:
APPLICANT: Agee, Wichele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Ference,
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Best Local Similarity:
Query Match:
                                                Alignment Scores:
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    JS-10-275-505-27
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91 ATTGTTGGGGGGCAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 150
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                                                                                                                                                                       25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeulleHisProGlnTrpValLeu
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                                                                                                     5 IleValGlyGlyGlyGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal
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                                                                    US-09-598-982-21 (1-249) x US-10-287-226-89 (1-828)
Mismatches:
Indels:
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Publication No. US20040086875A1
GENERAL INFORMATION:
APPLICANT: Agee, Michele L.,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Elsen, Andrew,
APPLICANT: Eisen, Andrew,
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95.51%
94.97%
Best Local Similarity:
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US-10-287-226-87
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APPLICANT: Rastelli, Luca,
APPLICANT: Rieger, Daniel K.,
APPLICANT: Rothenberg, Mark E.,
APPLICANT: Schenory, Suresh G.,
APPLICANT: Spaderna, Steven K.,
APPLICANT: Spytek, Kimberley A.,
APPLICANT: Taupier, Ur., Raymond J.,
APPLICANT: Taupier, Ur., Raymond J.,
APPLICANT: Carine A.M.,
APPLICANT: Carine A.M.,
APPLICANT: Schusen, Bryan D.,
APPLICANT: Schusen, Bryan D.,
APPLICANT: Schusen, Bryan D.,
APPLICANT: Carine A.M.,
APPLICANT: Carin
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SOFTWARE: CuraSeqList version 0.1
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Matches:
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PRIOR APPLICATION NUMBER: 60/334,421
PRIOR PLING DATE: 2001-11-30
PRIOR PLING DATE: 2001-11-30
PRIOR FILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-04
PRIOR PILING DATE: 2002-02-27
PRIOR PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/364,000
PRIOR APPLICATION NUMBER: 60/404,821
PRIOR PILING DATE: 2002-03-13
PRIOR PELING DATE: 2002-03-13
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PRILING DATE: 2001-04
PRIOR FILING DATE: 2001-04
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2002-03-13
PRIOR PILING DATE: 2001-11-30
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Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Miller, Isabelle,
                            Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
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1312.00
96.75%
96.75%
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Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ooi, Chean Eng,
Ort, Tatiana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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; LOCATION: (8)
US-10-287-226-87
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LENGTH: 858
                                                                                                                                                                            APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-09-598-982-21 (1-249) x US-10-287-226-87 (1-858)

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288 CGGGAGCACCTCTACTACTACCAGGACCAGCTGCCAGTCAGCAGGATCATCGTGCAC 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 ACCGCGCGCCACTGCCTGGGACCGGACGTCAAGGATCTGGCCACCTCAGGGTGCAACTG 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See File Wrapper or PALM.
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               FRIOR FILLING DATE: 2002-02-15
PRIOR FILLING DATE: 2002-03-15
PRIOR FILLING DATE: 2002-03-15
PRIOR FILLING DATE: 2002-04-26
PRIOR FILLING DATE: 2002-04-26
PRIOR FILLING DATE: 2002-06-06
PRIOR FILLING DATE: 2002-06-06
PRIOR PRILING DATE: 2002-06-24
PRIOR PRILING DATE: 2002-06-24
PRIOR PRILING DATE: 2002-06-28
PRIOR FILLING DATE: 2002-06-28
PRIOR FILLING DATE: 2002-06-28
PRIOR FILLING DATE: 2002-06-39
PRIOR FILLING DATE: 2002-07-31
PRIOR FILLING DATE: 2002-08-13
PRIOR FILLING DATE: 1002-08-13
PRIOR FILLING DATE: 2002-08-13
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1274.00
94.69%
92.24%
91.46%
   2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
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; LOCATION: (18)...(845)
US-10-352-684A-45
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspileAlaLeuLeuGluLeuGluGluPro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACAGTICTACACCGCCCAGAICGGAGCGGACAICGCCCCTGCTGGAGCTGGAGGAGCCG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAACGTCTCCAGCCACGTCCACACGGTCACCCTGCCCTGCCTCAGAGACCTTCCCC 481
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                                 122 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCTTGGCTGGGTGAGCTGAGGTC 181
                                                                                                                                                  CACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCCAGTGGGTGCTG 241
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                                                                                                                   HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
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408 GIGAACAICICCAGCGCGICCACACGGICAIGCIGCCCCCTGCCTCGGAGACCIICCCC 467
                                                                                                                                   ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla
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                                                                  CCGGGGATGCCCTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGATGATGACCCT
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APPLICANT: DELEGEANE, Angelo M.; LAL, Preeti G.
APPLICANT: HAFALIA, April J.A.; PATTERSON, Chandra
APPLICANT: HAFALIA, Narinder K.; KEARNEY, Liam
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: TASO, Monique G.; BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
APPLICANT: POLICKY, Jennitel B.; GANDHI, Ameena R.
APPLICANT: POLICKY, Jennifer L.; LU, Dyung Aina M.
APPLICANT: TANG, Y. TOM
APPLICANT: TANG, Y. TOM
TITLE OF INVENTION: PROFEASES
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; OTHER INFORMATION: Incyte ID No: 3897384CB1
US-10-275-505-22
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CURRENT APPLICATION NUMBER: US/10/275,505
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: PCT/US01/14651
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-05-01
PRIOR PLICATION NUMBER: 60/209,402
PRIOR FILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/205,803
PRIOR FILING DATE: 2000-05-17
PRIOR PLILNG DATE: 2000-05-17
PRIOR PLILNG DATE: 2000-05-11
PRIOR PLILNG DATE: 2000-05-04
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Publication No. US20040081961A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                               CysalaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
    588 AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGCTG 647
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                                                                                        APPLICANT: ANY Lasek
ITTLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
FILE REFERENCE: PA-0045 US
CURRENT APPLICATION NUMBER: US/10/116,802
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,593
PRIOR PILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 519
SOFTWARE: PERL Program
SEQ ID NO 240
LENGTH: 1158
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Mismatches:
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Matches:
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; OTHER INFORMATION: Incyte ID No: 378633.40
US-10-116-802-240
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323 AATGACACCTACAGGATGCATTTCTGCGGTGGCTCCCTCATCCACCACAGTGGGTGCTC 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
                                                                                                                      ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 104
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                                                                                                    | IleValGlyGlyGlnGluhlaProArgSerLysTrpProTrpGlnValSerLeuArgVal
                                                                                                                                             HisGlyProTyrTrpMetHisPheCysGlyGlySerLeulleHisProGlnTrpValLeu
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         1187
186
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         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                              Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Taupier Jr., Raymond J
APPLICANT: Majmuder, Kamud
APPLICANT: Spaderna, Steven K
APPLICANT: Smithson, Glenda
APPLICANT: Mezes, Peter S
         1.19e-119
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                            Percent Similarity:
Best Local Similarity:
Scores:
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TITLE OF INVENTION: No. CORING A. M.

TITLE OF INVENTION: No. CORING A. M.

FILE REFERENCE: 15966-729

CURRENT APPLICATION NUMBER: US/09/813,432

CURRENT FILING DATE: 2001-03-20

PRIOR PELICATION NUMBER: 60/190,935

PRIOR PELICATION NUMBER: 60/190,972

PRIOR PELICATION NUMBER: 60/190,972

PRIOR PELING DATE: 2000-03-22

PRIOR PELING DATE: 2000-03-22

PRIOR PELING DATE: 2000-03-22

PRIOR PAPLICATION NUMBER: 60/191,947

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-28

PRIOR PELING DATE: 2000-03-38

PRIOR PELING DATE: 2000-03-39

PRIOR PELING DATE: 2000-03-39
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241 IleHisHisTyrValProLysLysPro 249
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Search completed: July 22, 2004, 19:33:58 Job time: 526 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 22, 2004, 14:36:26; Search time 83 Seconds (without alignments) 946.555 Million cell updates/sec

US-09-598-982-21 1393 1 LEKRIVGGQEAPRSKWPWQV.....IYTRVTXXLDWIHHYVPKKP 249 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1017041 seqs, 315518202 residues Searched:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: Sp\_archea:\*

2: Sp\_bacteria:\*

3: Sp\_fungi:\*

4: Sp\_human:\*

5: Sp\_invertebrate:\*

7: Sp\_mhc:\*

8p\_organelle:\*

8p\_organelle:\*

8p\_page:\*

9p\_page:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	O96rz6 homo sanien	O86tm8 homo sanien	homo	O7vs62 emins cabal	OShvi2 hos taurus	092184 1118 1118 1111	O96rz7 homo sanien	O9xsm1 ovis aries	029464 hos taurus	0801r4 mis miscilli	OBSE44 SIS SCROFA	099ms4 mils milscril	Ulticalim sim Shirt	Ogerze homo ganien	OBOWE 2 MONTH BUILD	Q924n9 mus musculu
SUMMARIES		QI .	Q96RZ6	Q86TM8	Q86UA5	Q7YS62	O8HYJ2	0921N4	Q96RZ7	O9XSM1	029464	O80UR4	08S044	099MS4	OBBJR6	O96RZ8	O80WM7	Q924N9
		DB	4	4	4	9	9	H	4	9	9	11	9	11	11	4	11	11
		Match Length DB	275	275	276	275	271	273	233	273	237	318	277	279	328	321	277	274
	* Query	Match	96.3	92.3	92.3	78.4	75.4	75.1	73.4	73.2	72.1	48.7	46.7	45.9	42.8	42.3	42.2	40.8
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## ALIGNMENTS

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5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
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                                                                        VPKKP 249
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                                                                                                                          REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                   REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFP 150
                                                                                                                                                                                                   151 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 210
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                                                                                         31 IVGGQEAPRSKWPWQVSLRVHDPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQL 90
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                        96.3%; Score 1342; DB 4; Length 275; 98.0%; Pred. No. 2.4e-123; ive 0; Mismatches 5; Indels (
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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2F4AAAAE7DDE483E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Interpro; IPR001254; Peptidase_S1.
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PRINTS; PRO0722; CHYMOTRYPSIN.
PROSTE; SMO0020; TYP, SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN FIS; 1.
SEQUENCE 275 AA; 30713 MW; 189C3
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  275 AA; 30601 MW;
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93.5%;
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                                       Best Local Similarity
                                                    Matches 240;
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MEDLINE-22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atausberg R.L., Feingold E.A., Grouse L.H., Schaefer G.D.,

Ataschul S.F., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Atschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Antschenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

As Diatchenko L., Gadin T.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

As Atapleton M.J., Jodin T.B., Ponaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.B.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Ashoriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rhakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhakesley R.W., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Romes S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
151 PGMPCWVTGWGDVDNDEPLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIIRDDML 210
                                                                                                                                    211 CAGNIRRDSCQGDSGGPLVCKVNGTWLQAGVVSWDBGCAQPNRPGIYIRVTYYLDWIHHY
                                                                                        CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BCOG1823; F:chymotrypsin activity; IEA.
GO; GO:0004233; F:chymotrypsin activity; IEA.
GO; GO:0004285; F:trypsin activity; IEA.
GO; GO:0006289; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
Ffam; PR00839; trypsin; 1.
RMRI; R00020; Tryp SPC; 1.
RMRI; S00020; Tryp SPC; 1.
RROSITE; PSC0134; TRYPSIN DOM; 1.
RROSITE; PSC0134; TRYPSIN JHS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.3%; Score 1286; DB 4;
93.5%; Pred. No. 7.4e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similar to tryptase, alpha (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-070-2003 (TrEMBLrel. 24, Created)
01-070N-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                       PGMPCWVIGWGDVDNDEPLPPPFPLKQVKVPIMENHICDAKYHLGAYIGDDVRIIRDDML 211
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                                                                               REQHLYYQDQLLPVSRIIVHPQFYIIQTGADIALLELEEPVNISSRVHTVMLPPASETFP 151
                                                                                                                 PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                   CAGNIRRDSCQGDSGGPLVCKVNGTWLQAGVVSWDEGCAQPNRPGIYTRVTYYLDWIHHY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 RDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
32 IVGGQEAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLJTAAHCLGPDVKDLATLRVQL
                                                                                                                                                                                CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Dacter K.J., McAlesses S., Pemberton A., McGorum B.C.,

"CDMA sequence of two equine mast cell proteases and the differential expression of tryptase and equine mast cell protease-1 in equine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LEKR-IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The role of mast cells and mast cell proteases in equine heaves."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AJ515902; CAD56807.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

78.4%; Score 1092.5; DB 6; Length 275;
Best Local Similarity 77.8%; Pred. No. 7.1e-99;
Matches 193; Conservative 19; Mismatches 35; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA; 30476 MW; 718F57A4DBEE21ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tryptase (EC 3.4.21.59). MTC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Horse)
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266 WIYQYVPK 273
                                                                                                                                                                                                                                             245 VPKKP 249
                                                                                                                                                                                                                                                                            VPKKP 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 PGMPCWVIGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 IVGGQEAPGSRWFWQVSLRVSRRYWRHHCGGSLIHPQWVLTAAHCVGPEVHGPSYFRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 REQHLYYQDQLLDISKIIPHPNYYSVKNGADIALLELDKLVNISWHVQLVTLPPESETFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 PGTQCWVTGWGNVDNGRRLPPPFPLKQVKVPVVENSVCDRKYHSGLSTGDNVSIVQEDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                             TISSUE-Lung;
Gambacurta A., Fiorucci L.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AFS15641; AAN77096.1; -.
PIR; S24190; S24190.
GO; GO:0004295; Firrypsin activity; IEA.
GO; GO:0006509; P; Proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                 Pram; Productors; 1. Swart; 2. Swart; 5M00020; trypsin; 1. PROSITE; PS001240; Tryp_SPC; 1. PROSITE; PS00134; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSIN_HIS; 1. SEQUENCE 271 AA; 29902 MW; 1B68B5A18BA80CFA CRC64;
                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.4%; Score 1051; DB 6; 75.9%; Pred. No. 8.2e-95; tive 22; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 186; Conservative
                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mast cell protease 7. MCPI7.
                                                                                                                                         Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                            Tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                             Q8HYJ2
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RESULT 5
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGNEGHDSCQGDSGGPLVCKVEDTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHRY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGNTRRDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 IVGGQEAHGNKWPWQVSLRANDTYWMHFCGGSLIHPQWVLTAAHCVGPDVADPNKVRVQL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16.";
Hum. Mol. Genet. 10:339-352(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
BENBL; AEGO6466; AAK61270.1; -.
HSSP; P00761; LANI.
GO; GO:0004263; F:chymotrypsin activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINS=21086910; PubMed=11157797;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.1%; Score 1046; DB 11; Length 273; 76.1%; Pred. No. 2.6e-94; Indels 0;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-:-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BCO11328; AAH11328.1; ---
R HSSP; P00761; 1AN1.
R MGD; MGI:96943; MCPt7.
R GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0008235; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:chymotrypsin activity; IEA.
R GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:0004295; F:trypsin activity; IEA.
R InterPro; IPR001354; Peptidase_S1.
R InterPro; IPR001354; Peptidase_S1.
R Ffam; PF00089; Lrypsin; I.
R PROSTTS; PR00722; CHYMOTRYPSIN.
R PROSTTS; PS00135; TRYPSIN DOM; I.
R PROSTTE; PS00134; TRYPSIN DOM; I.
R PROSTTE; PS00135; TRYPSIN DOM; I.
R PROSTTE; PS00135; TRYPSIN LIS; I.
R PROSTTE; PS00135; TRYPSIN LIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Protease; Serine protease.
SEQUENCE 273 AA; 30332 MW; 51417476514035BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096R27;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell tryptase beta III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 76.1
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 VPK 247
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196RZ7
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AC 096R
AC 096R
DT 01-D
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DT 01-O
DT MAST
COC MANN
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RN [1]
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RA HIGG
RA HIGG
RT NSC
RT NS
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91 REGHLYYODOLLPVSRIIVHPOFYTAQIGADIALLELEEPVNVSSHVHTVTLPPASETFP 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 IVGGOEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
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-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.4%; Score 1022; DB 4; Length 233; 97.4%; Pred. No. 4.8e-92; tive 0; Mismatches 5; Indels C
GG; GG:0008233; F; peptidase activity; IEA.

GG; GG:0004295; F: trypsin activity; IEA.

GG; GG:0005508; P: proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

R PRIMY: PR00089; trypsin; 1.

R PRIMY: PR00020; Tryp SPC; 1.

R PROSITE; SS0240; TRYPSIN LOM; 1.

R PROSITE; PS0134; TRYPSIN HIS; 1.

R PROSITE; PS0134; TRYPSIN HIS; 1.

Hydrolase; Protease; Serine protease.
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GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0030019; F:tryptase activity; IEA.
GO; GO:00508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR00103; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
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MEDLINE=20308142; PubMed=10848900;
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y18223; CAB41988.1; -- HSSP; P20231; 1A0L.
MEROPS; S01.118; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 186; Conservative
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Protease.
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SEQUENCE
                       Query Match
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                                                                                                                             64
                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "CDNA cloning and primary structure of tryptase from bovine mast cells and evidence of the expression of bovine pancreatic trypsin inhibitor mRNA in the same cells."

Eur. J. Biochem. 237:100-105(1996).

-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                          29 IIGGKEAPGSRWPWQVSLRVRDQYWRHQCGGSLIHPQWVLTAAHCIGPELQBPSDFRVQL
                                                                                                                                                                            65 REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP
                                                                                                                                                                                         PGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDML
                                                                                                                                                                                                                                         149 PGSQCWVTGWGNVDNGRPLPPPYPLKQVKVPIVENSVCDWKXHSGLSTDYSVPIVQEDNL
                                                                                                                                                                                                                                                                              CAGNTRRDSCOGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHY
                                                                                                                          5 IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQL
                                                                                                  Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-Yptase (EC 3.4.21.59) (Fragment).
Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pallaoro M., Gambacurta A., Fiorucci L., Mignogna G., Barra D.,
                                                                                                  .;
0
                                                                         h 73.2%; Score 1019; DB 6; Length 273; Similarity 71.8%; Pred. No. 1.1e-91; 76; Conservative 29; Mismatches 40; Indels
                                                  SEQUENCE 273 AA; 30156 MW; 88A19DC779053898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; 20131; 1A0L.
MEROPS; S01.118;
O) G0:0004263; F:chymotrypsin activity; IEA.
G0; G0:000823; F:peptidase activity; IEA.
G0; G0:003019; F:tryptase activity; IEA.
G0; G0:0006808; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                      237 AA
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS000134; TRYPSIN HIS; 1.

Hydrolase; Protease; Serine protease.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
CHAIN 29 273 TRYPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=96203914; PubMed=8620861;
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                                                                                                    Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S68702; S68702.
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                                                                                                                                                                                                                                                                                                                                                         269 VPQEP 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 WGNVDNGRRLPPPFPLKQVKVPVVENSVCDRKYYSGLSTGDNVPIVREDMLCAGDSGRNF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 QLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 QLLPISRIIPHPNCYSVKNGADIALLELDKLVNISWHVQPVTLPPESETFPPGTQCWVTG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 WGDVDNDERLPPPFFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDS 193
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                                                                                                                                                                                                                                                                                                                                                       14 SKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALRVQLREQHLYYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 CQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 CQGDSGGPLVCKVNGTWLQAGVVSWGDGCAKPNRPGIYTKVTSYLDWIHQYVPQGP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                        Length 237;
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EMBL; AYZ61775; AAP21675.1; -.
GO; GO:0004263; F:chymotryppin activity; IEA.
GO; GO:0008429; F:peptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
EnterPro; IPR001254; Peptidase S1.
EnterPro; IPR001254; Peptidase S1.
EnterPro; IPR001254; Peptidase S1A.
Ffam; PF00089; trypsin; 1.
FRINTS; PR0020; Tryp SDF; 1.
FRINTS; PR00144; TRYPSIN D0M; 1.
FROSITE; PS00134; TRYPSIN D18; 1.
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                                                                                                                  72.1%; Score 1005; DB 6; Length 2: 75.4%; Pred. No. 2.3e-90; ive 21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA; 35037 MW; 6F69B6653FF54FEA CRC64;
237 AA; 26550 MW; EA537A75294EFFBA CRC64;
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01-UDN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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48.7%; Score 678; DB 11;
Best Local Similarity 52.4%; Pred. No. 3.9e-58;
Matches 130; Conservative 37; Mismatches 75;
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                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                        Best Local Similarity
Matches 178; Conserv
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241 I 241
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                                                                 099MS4;
                                                    Q99MS4
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                             RESULT 12
                                         Q99MS4
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                     179 VRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYL 238
                                  215 IKDDMLCAGKEGRDSCKADSGGPLVCRWNCSWVQVGVVSWGIGGCLPDFPGVYTRVMSYV 274
155 ASLRISSKKTCWVAGWGVIENYMPLPPPYHLREVAVPIVENNDCEQKYQTNSSSDSTTRI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 VQLREQHLYYQDQLLPVSRIIVHPQFY-TAQIGADIALLBLEEPVKVSSHVHTVTLPPAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ETFPPGMPCWVTGWGDVDNDERLPPFFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 DDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGBGCAQPNRPGIYTRVTYYLDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 ADMLCAGSKGLDSCQGDSGGPLMCSWNGTWVQVGIVSWGRGCGLHNFPGVYIRVMSYVSW 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IVGGQEAPRSKWPWQVSL---RVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKDLAALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                   Sato M., Yoshida S., Iida K., Tomozawa T., Kido H., Yamashita M., "A Novel Influenza A Virus Activating Enzyme from Porcine Lungs: Purification and Characterization.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB080655; BAB85761.1; -.
                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
46.7%; Score 651; DB 6; Length 27
Best Local Similarity 50.6%; Pred. No. 1.5e-55;
Matches 126; Conservative 39; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                          GO: GO:000426; F:chymotrypsin activity; IEA.
GO: GO:000429; F:chymotrypsin activity; IEA.
GO: GO:0004295; F:chypsin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
InterPro; IPR00126; Peptidase_S1.
InterPro; IPR00124; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Ffam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SNART; SM00020; Tryp SPC; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 AA; 30407 MW; 35FC8B569C0ED4C5 CRC64;
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Last annotation update)
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                                                                                                                                                                                     Created)
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                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                            PRELIMINARY;
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                                                                     239 DWIHHYVP 246
                                                                                               275 SWIKCYVP 282
                                                                                                                                                                                                                     Tryptase precursor.
Sus scrofa (Pig).
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62 VQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASE 121
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MEDLINE=21361749; PubMed=11467974;
O'Sullivan C.M., Liu S.Y., Rancourt S.L., Rancourt D.B.;
"Regulation of the strypsin-related proteinase ISP2 by progesterone in endometrial gland epithelium during implantation in mice.";
Reproduction 122:235-244(2001).
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                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Uterus;
Shen O.-X., Wang J., Huang Z.-P.;
"Identification of endometrial factors involved in mouse embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.9%; Score 640; DB 11; Length 279;
49.8%; Pred. No. 1.8e-54;
tive 36; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO: 0004255; F: chymotrypsin activity; IEA.
GO; GO: 0004295; F: chymotrypsin activity; IEA.
GO; GO: 0004295; F: trypsin activity; IEA.
GO; GO: 0006208; P: proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cye_Ser_trypsin.
InterPro; IPR00134; Peptidase_S1.
InterPro; IPR00134; Trypsin, 1.
INTERPRO; PR00122; CHYMOTRYPSIN.
INTERPRO; PR00134; TRYPSIN DOM; I.
IPROSITE; PS00134; TRYPSIN DOM; I.
IPROSITE; PS00134; TRYPSIN HIS; I.
IPROSITE; PS00135; TRYPSIN ER; I.
INTERPROSITE; PS00135; TRYPSIN ER; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 implantation.";
Submitted (NOV-201) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AF305425; AAK12264.2; -.
HSSP; OF0763; 1DPO.
HSSP; S01.315; -.
                                ou-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:2149952; ISp2.
                                                                                                                                                                                                  (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120;
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117 PPASETFFPGMPCWVTGWGDVDNDERLPPPFFLKQVKVPIMENHICDAKYHLGAYTGDDV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase, Protease, Serine protease, Transmembrane.
SEQUENCE 321 AA, 33829 WW, FFF5089EDC4FC73D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
HS transmembrane tryptase, gene name TMT, AF175522_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GG; GG:0016021; C:integral to membrane; IEA.
GG; GG:0004263; F:chymotrypsin activity; IEA.
GG; GG:0004233; F:peptidase activity; IEA.
GG; GG:0004295; F:trypsin activity; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009033; Cys. Ser_trypsin.
InterPro; IPR001314; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                      321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                      PRT;
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PRINTS; PR00722; CHYMOTRYPEIN.
PRART; SM0020; Tryp_SBC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.48;
                                                                                                                                                                                              TYYLDWIHHYVPK 247
                                                                                                                                                                                                                                          269 TSHHKWIHQIIPE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00761; 1AN1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Higgs D.R.;
                                                                                                                                                                                              235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Q96RZ8;
                                                                                                                                                                                                                                                                                                                                                                      096RZ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEFVKVSSHVHTVTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Thymus; MEDLINE=22354683; WEDLINE=22354683; PubMed=1246683; The PANTOM CONSOrtium the RANTOM CONSOrtium Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 RIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAACVGPDVKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and activity of human pancreasin, a novel tryptic serine
                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to MARAPSIN precursor (Channel-activating protease 2-like
                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6; TISSUE=Bladder;
MEDLINE=22439795; PubMed=12441343;
Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Wolters P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genomic Sequence Analysis in the Mouse T-complex Region."; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129S6/SvEvTac;
Brathwaite M., Waeltz P., Schlessinger D., Nagaraja R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:2450123; Mpn.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006509; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidase expressed primarily by the pancreas.";

J. Biol. Chem. 5:3363-3371 (2003).

EMBL; AK080281; BAC37864.1; -.

EMBL; AX162410; AAO17162.1; -.

EMBL; AF542056; AAO27572.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp, SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN ES; 1.
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                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                      protein) (Pancreasin).
                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caughey G.H.;
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                                                                                                                      QBBJR6
                                                                     RESULT 13
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                                                                                                                209 KTIKDDMLCAGFAEGKKDACKGDSGGPLVCLVDQSWVQAGVISWGEGCARRNRPGVYIRV 268
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149 PDPSVIFESGMNCWVIGWGSPSEQDRLPNPRVLQKLAVPIIDTPRCNLLYNKDVESDFQL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 DFCPGIRCWVTGWGYTREGEPLPPPYSLREVKVSVVDTETCRRD-----YPGPGGSILQP
                                                                           177 RIVRDDMLCAG--NTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 RIVGGHAAPAGAWPWQASLRLRR----VHVCGGSLLSPQWVLTAAHCFSGSLNS-SDYQVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 DMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVIYYLDWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence, structure and pathology of the fully annotated terminal Mb of the short arm of human chromosome 16.";

Hum. Mol. Genet. 10:339-352(2001).

EMBL, AEOLOGS TO PEPTIDASE FAMILY S1.

EMBL, AEOLOGS AAK61269.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21096910; PubMed=11157797;
Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 TLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGD 174
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.

STRAIN=BALB/C; TISSUE-Testis;

STRAIN=BALB/C; TISSUE-Testis;

Wong G.W., Yasuda S., Li L., Stevens R.L.;

"Cloning and characterization of mouse tryptase-6 (mT6).";

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY262280; AAP20885.1; -.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R GO; GO:0004295; F:trypsin activity; IEA.

R InterPro; IPR00134; Peptidase_SIA.

InterPro; IPR00134; Peptidase_SIA.

R Ffan; PF000722; CTYPD-SPC; 1.

R RNNTS; RN00722; TYMVTYEN.

R RNSTT; SN0020; TTYP_SPC; 1.

R RNSTTE; PS00134; TRYPSIN_DN; 1.

R RNSTTE; PS00134; TRYPSIN_SER; 1.

R RNSTTE; PS00134; TRYPSIN_SER; 1.

R RNSTTE; PS00135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                              277 AA
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242 HHYV 245
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Search completed: July 22, 2004, 15:25:07 Job time : 85 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein - nucleic search, using frame\_plus\_p2n model

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July 22, 2004, 15:33:07; Search time 3069 Seconds (without alignments) 2422.836 Million cell updates/sec Run on:

1393 1 LEKRIVGGOBAPRSKWPWQV.....IYTRVTYYLDWIHHYVPKKP 249 0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-598-982-21 **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-O=/Cqn2 1/USPTO spool p/US09598982/runat 20072004 064410 6500/app query.fasta\_1.391
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO MMAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:\* Database :

em\_gss\_inv:\*
em\_gss\_pln:\*
em\_gss\_vrt:\*
em\_gss\_fun:\* em\_gss\_pro:\*
em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* em gss mam:\* em\_gss\_mus:\* em\_gss\_hum:\* em\_esthum:\*
em\_estin:\*
em\_estcv:\*
em\_estpl:\*
em\_estpl:\*
em\_estro:\*
em\_htc:\*
gb\_est1:\* em\_estfun:\* em\_estom:\* gb\_est3:\* gb\_est4:\* 1: em\_estba:\* gb\_est2:\* gb\_est5:\* gb\_htc:\* 1112... 1122... 1144.. 10:

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	919268 AGENCO	0404	/1/33 1m33a09	1851 19	712600	718917	10689	1892 BX09	97540	32929 K-ES	37772	2089	3026	CF553058 AGENCOURT	1078	3263	3025	142	591	0425	937 uf61	3801	1180 bx01	8721 UI-H	81986 Mus musc	39686 UI-H-DTI	361 UI-H-E11	91728 UI-H-DFI	BMS89945 OI-H-DIO	SOO MUS	130 QV5-E10	54077 6028288	308	90168	m 0806	52270	75716 468400	31216 4605	80281 Mus m	46157 CH240	A867461 ir28£	E751979 204246	87271 UI-	
DB ID	1926	BQ7204	BU0717	4 CD6/18	B14132	4 CD203 4	CD6726	3 BX0918	2 BG6975	B00829	13 BU787772	BG5420	4 CF5830	4 CF5530	3 BQ7210	3 BU0732	14 CF583025	AA13114	2 BG4835	4 CB8404	0 AW8239	2 BI7908	0 BF7241	4 CA4387	1 AK0819	4 CA4396	2 BQ0033	2 BM9917	Z BM9895	AKO402	120011	2 RG964C	0 BF85	4 CB5891	AA04908	0 BE86227	757	2 BI68121	1 AK08028	CC54615	4 CA867	BE75197	BI28727	
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# ALIGNMENTS

AGENCOURT\_6715837 NIH\_MGC\_120 bp mRNA linear EST 12-WAR-2002 S, mRNA Fequence. BM919268.1 GI:19369647 Homo sapiens (human) Homo sapiens LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE BM919268 RESULT 1

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1030)

REFERENCE

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/mol_type="mRNA"
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BQ720404
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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size range 1-2:5 kb. insert size range 1-2:5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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        ProProPheProLeuLysGlnValLysValProIleMetGluAsnHis1leCysAspAla 164

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
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                                                                           Email: cgapberformal.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Flate: LiAMA12776 row: f column: 20
High quality sequence stop: 719.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                          clone lib="NIH_MGC_120"
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1263.00
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AGENCOURT 8477973 Lupski sympathetic_trunk Homo sapiens cDNA clone IMA6E:6196776 5', mRNA sequence.
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543 CCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 602
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                          205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGly--GluGlyCysAlaG
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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M. A.G. E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M. A.G. E. Consortium/LLNL at:
http://mage.llnl.gov. m column: 01
                                                                                                                                                                                                                                                                                                                                                                185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
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/note=_organ: parcreas; Vector: pBluescript SK-; Site_1:
Xhoi; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
laboratory, Washington University School of Medicine, Box
Black Go S Bullid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
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                                                                                                                                                                                                                                                            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
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                                                                                                                                                                                                                                                                                                                                       Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@blohp.harvard.edu
Enail: dmelton@blohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining in Colore please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 433.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schaltt,A., Thelsing,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGCGGACATCGCCCTGCTGGAGCTGGAGCCGGTGAACGTCTCCAGCCACGTCCAC
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                                                                                                                                                                      Other_ESTs: im33a09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                 Endocrine Pancreas Consortium Unpublished (2000)
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1062.00
99.48%
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ORIGIN Alignment Scores: 7.95e-97 Length: 619 Pred. No.: 1060.00 Matches: 3 Best Local Similarity: 92.68\$ Mismatches: 12 Ouery Match: 14.09\$ Indels: 0 DB:	US-09-598-982-21 (1-249) x CD671851 (1-619)  Qy	AlaCysValGlyProAspValLySAspLeuAlaAlaLeuArgValGlnLeuArgGluGln [   :::	88 TyrThrAlaGlnIleGlyAlaAspileAlaLeuLeuGluLeuGluGluProValLysVal 107  243 TACATCATCAGGGGGGATATCGCCCTGCTGGGGGGGGCCCGTGAACATC 302  108 SerSerHisValHisThrValThrLeuProProAlaSerGluThrPheProProGlyMet 127	ProLeuLysGlnVall	RESULT 5  RESULT 5  RESULT 5  RESULT 5  RESULT 5  B1413250  LOCUS  LOCUS  LOCUS  LOCUS  B1413250  LOCUS  B1413250  B141320  B1413250  B1
ORIGIN Alignmer Pred. Nc Score: Percent Best Loc Query Ms	08-00 07 OY	6 6 6	8 6 6 6 6	8 8 8 8 8 8	RESULT 5 B1413250 LOCUS DEFINITIC ACCESSION VERSION VERYWORDS SOURCE ORGANIE REFERENCE AUTHORS
153 LysValProileMetGluAsnHisTleCysAspAlaLysTyrHisLeuGlyAlaTyrThr   172	213 AladlyValValSerTrpGlyGluGlyCysAlaGlnProAsnArgProGlyIleTyrThr 232	RESULT 4  CD671851 CD671851 CD671851 CLOUS CD671851 CLOUS CD671851 CLOUS CD671851 CLOUS CD671851 CD671	×	PUBMED 12107412  COMMENT CONTACT: Wistow G  Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 496 0078 Fax: 304 496 0078 Email: graeme@helix.nih.gov Plate: 07 row: g column: 11 Seq primer: M13RP1 reverse primer (ABI). FEATURES 1. 619 //organism="Homo sapiens" //db_xref="Homo sapiens" //db_xref="Homo sapiens" //db_xref="Homo sapiens" //db_xref="Homo sapiens" //db_xref="Homo sapiens"	/close='rgo'gll." /tissue type='Iris" /dev_stage='Adult." /lab_host='EMBHIOS" /lab_host='EMBHIOS" /clore lib='Human Iris cDNA (Normalized): fg" /clore lib='Human Iris cDNA (Normalized): fg" /clore lib='Human Iris cDNA (SPORTE; A human iris /note='Organ: Eye; Vector: pcNVSPORTE; A human iris /note='Organ: Eye; Vector: pcNVSPORTE; A human iris /note='Organ: Eye; Vector: pcNTION iris /note='Organ: Exranded plasmid blasmid DNA representaing the /normalized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SPE RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural

734

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Norteal Vector: DCMVSport6.1; Site 1: EcoRV; Site 2: Not1; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dr. cDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb, Priming sequence: S'GACTRGTTCTRGATCGCGAGGCGCCCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 05-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                          224 ln-ProAsnArgProGly1leTyrThrArgValThr-TyrTyrLeuAspTrp1leHisHi 243
                                                                                                                                                                                                                                                                                                                                                                                    614
ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 930)
                                                                                                                                                                                                               615 GIGTGCTGGAAATACCAGGAGAGACTCCTGCCAGGGCGATTCAGGGGGGCCACTGGTCTG
                                                                                                                                  555 Aagraaccacacrescercracacsesasarsarrreccarisrecarsarsserieer
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                                                                                        Lys-TyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspAspMetLe
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue procurement: Dr. David Rowe
Tissue procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: NDAMOSI row: j column: 17
High quality sequence stop: 681.
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AGENCOURT 11288628 NIH MGC 135 Mus musculus cDNA clone IMAGE:30142408 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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Mus musculus
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Pred. No.:
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TITLE
JOURNAL
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SOURCE
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CB203717
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                                                                                                        Duracto, Full

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMIJ351 row: c column: 23

High quality sequence start: 32

High quality sequence stop: 849.
                                                                                                                                                                                                                                                                                                                                                                               Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 VallysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 ATCGTGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGATTT 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 ACTGCGGCACACTGTGTGTGGGACCGCACAAAAGCCCACACACTCTTCCGGGTGCAGCTT
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                                                                        Σ.
                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D.
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Matches:
Conservative:
Mismatches:
Indels:
                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
      Contact: Robert Strausberg, Ph.D.
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Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
Mol. Vis. 8 (4), 185-195 (2002)
                                                                                                                           Section on Molecular Structure and Function
                                                                                                                                    National Eye Institute 6/33, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 08 row: b column: 10 Seq primer: M13RP1 reverse primer (ABI).
                                                                                                              Contact: Wistow G
                                                                                                12107412
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                                                                     JOURNAL
MEDLINE
PUBMED
    AUTHORS
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                                                                                                                                                                                            161
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                                                                                                                                                                                                                                                                                        ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluGluPro 104
                                                                                                                                                                                                                                                                                                                                                                                                     ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGACATCGTGCTGGTGACAGGCTGGGGCGACATTGATAATGACGAGCCTCTCCCA 461
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                                                                                                                                                                                                                                                                                                                                             25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeulleHisProGlnTrpValLeu
                                                                                                                                                                                         102 AAATTAAACTACTIGGATACATTICTGCGGAGGCTCTCTCTCATCCACCCACAGTGGGTGCTC
                                                                                                                                                                                                                      ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu
188
19
36
4
              Conservative:
Mismatches:
Indels:
 Matches:
                                                      Gaps:
                                                                                (1-930)
                                                                             US-09-598-982-21 (1-249) x CB203717
1023.00
83.81%
76.11%
73.44%
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           Percent Similarity:
Best Local Similarity:
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/organism="Homo sapiens"

j. .635

/mol\_type="mRNA" /db\_xref="taxon:9606" /clone="fg08b10"

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/tissue type="Itis"
/day stage="Adult"
/dab_host="Emplion"
/dab_host="Emplion"
/done lib="Human Iris cDNA (Normalized): fg"
/done lib="Human Iris cDNA (Normalized): fg"
/done lib="Human Iris cDNA (Normalized) & human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exomuclasse III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(CDC 500) with 41 mg of Bio-RNA and vector blocking
oligomotleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NH Intramural
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Mismatches:
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Best Local Similarity:
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DP ò

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 635)

Homo sapiens (human)

sapiens

ORGANISM

REFERENCE

ACCESSION VERSION KEYWORDS SOURCE

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Query Match:
DB:
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/clone="fag15a06"
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/dev_stage="Adult"
/lab_host="EmbH10B"
/clone_lib="Human Iris cDNA (Normalized): fg"
/clone lib="Human Iris cDNA (Normalized): fg set family 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fg15a06.y2 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone fg15a06 5', mRNA sequence.
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(Dases 1 to 642)

Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A., Touchman,J."W., Bouffard,G., Smith,D. and Peterson, K.

Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear EST 24-JUN-2003
                                                             456
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                                    397 GIGAACGICICCAGCCACGICCACACGGICACCCCTGCCCCTGCCTCAGAGACCTICCCC
                                                                                                                    ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro
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ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro
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Section on Molecular Structure and Function
National Eye Institute
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Plate: 15 row: a column: 06
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mol. Vis. 8 (4), 185-195 (2002)
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Fax: 301 496 0078
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Alignment Scores:

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BX091892
BX091892 Soares fetal liver spleen INFLS Homo sapiens cDNA clone INAGP998M0584; IMAGE:110380, mRNA sequence.
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Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Umpublished (2003)
Contact: Ina Rolfs
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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RZPDLJB, I.M.A.G.E. CDNA Clone Collection;
Human UniqueneSet - RZPDJ3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Ggi-
                                     Conservative:
Mismatches:
                   Matches:
Length:
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BG697540 811 bp mRNA linear EST 07-MAY-2001
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/clone lib="NCI CGAP SRN3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
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/ste_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics. Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM.0700 row: g column: 16
High quality sequence stop: 781.
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Conservative:
Mismatches:
Indels:
GACTGGATCCACCACTATGTCCCCCAAAAAGCCG 513
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Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                                                                          mRNA sequence.
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BG697540
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TITLE
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                                                                               www.rzpd.de
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
Ml3r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                           /mol_type="mRNA"
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/clone="IMAGp998M0584; IMAGE:110380"
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/organism="Homo sapiens"
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105 VallysvalSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124 400 GTGAAGGTCCCAGCCACACACACACACACACACACACACA		Tel: +82-42-860-4470 Fax: +82-42-860-4470 Fax: +82-42-860-440 Email: yongsung@mail.kribb.re.kr Plate: 59 row: B column: 11 High quality sequence stop: 502. Location/Qualifiers 1502
0y 100 0y 400 0y 122 0y 141 0b 522 0y 146 0y 146 0y 146 0y 166 0y 166 0y 166 0y 166 0y 166	RESULT 11 BQ082929 LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES

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adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUT87772 581 bp mRNA linear EST 11-OCT-2002 io34c08.yl Human insulinoma Homo sapiens cDNA clone IMAGE:6128247 5' similar to SW:TRYB_HUMAN P20231 BETA-TRYPTASE PRECURSOR ;, mRNA
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1 (Dases 1 to 581)
Melton, D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
                                                                                                                                                                                                                                                                                                                                                                                                  28 TyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeuThrAlaAla
2 TACTGGATGCACTTCTGCGGGGGGTCCCTCATCCACCCCCAGTGGGTGCTGACCGCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AACACCCGGAGGGACTCATGC 502
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BU787772.1 GI:23835713
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/Mol type="mRNA"
//db_xref="taxon:9606"
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/lab host="MARA"
/clone="INABRA"
/clon
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602571309F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695458 5',
                                                       506 CCGCCATTTCCTCTGAAGCAGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 736)
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Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
Plate: LLCM1521 row: b column: 03
High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                            ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla
                                                                                                                                       ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro
                                                                                                                                                                                                                        446 CCGGGGGATGCCGTGCTGGGTCACTGGCTGGGCCGATGTGGACAATGATGAGGCGCCTCCCA
            NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     736
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Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt inaboratory, Meshington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:6128247"
/tissue type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="PH10B (phage-resistant)"
/clone lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
/knot; Site_2: BcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
//niversity protocol
                                                                                                                                                            Unpublished (2000)
Cherr ERTS: 1034c08.XI
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Endocrine Pancreas Conso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeulleHisProGlnTrpValLeu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining Seq primers contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IleValGlyGlyGluGluAlaProArgSerLySTrpProTrpGlnValSerLeuArgVal 24
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Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biobp.harvard.edu
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/db_xref="taxon:9606"
                                                                                                                               Endocrine Pancreas Consortium
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/note="Organ: parcreas; Vector: pSPORTI; Site 1: Sall; Site_2: NotI; Library consists of a pool of clones rearrayed from the following libraries: Melton normalized mixed mouse pancreas 1 NI-PMSI, Amplified Melton mouse islets 1 MISI-A, and Kaestner om 3 wt. Clones rearrayed in the laboratory of K. Kaestner (University of Pennsylvania). Note: this is a NIH_MGC Library."
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929 bp mRNA linear EST 24-SEP-2003
AGENCOURT_8786077_updated NIH MGC_137 Mus musculus cDNA clone
IMAGE:6432257 3', mRNA sequence.
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                                                                                                         CACGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTG 234
                                                                                                                                                                                      ACCGCAGCGCACTGCGTGGGACCGTCAAGGATCTGGCCGCCCTCAGGGTGCAACTG 294
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov.h column: 06
Plate: IRBD24 row: h column: 06
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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Search completed: July 22, 2004, 18:14:21 Job time : 3075 secs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                            CF553058
AGENCOURT 15594982 NIH_MGC_183 Homo sapiens cDNA clone
IMAGE330529468 5', mRNA sequence.
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159
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17
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: GRM10A07 Bethesda, MD 20892
Fisil: GRM10A05-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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High quality sequence stop: 611.
Location/Qualifiers
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428 CGGGAGCAGCACTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCAC 487
                                                                                                                                    488 CCACAGTTCTACATCATCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGCCC
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model Run on:

July 22, 2004, 10:05:00 ; Search time 5131 Seconds (without alignments) 6512.859 Million cell updates/sec

1 gggcccctcgagaaaagaat....... US-09-598-982-20 Perfect score:

Scoring table: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

3470272 segs, 21671516995 residues

Searched:

6940544 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

gb ba: \*
gb htg: \*
gb htg: \*
gb ow: \*
gb ov: \*
gb pt: \*
gb pt: \*
gb pt: \*
gb v: \*
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gb v: \*
em ba: \*
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em\_in:\*
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em\_pl:\* em\_ro:\* em\_sts:\* em un:\*

em\_vi:\* em\_htg\_hum:\* em\_htg\_inv:\*

em\_htg\_other:\*
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em\_htg\_rod:\*
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em\_htg\_vrt:\*

em\_htgo\_mus:\* em\_htgo\_other:\* em\_htgo\_hum: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ion	3X347953 Computer		7062 Sequence	47841 Sequence	11490 Enzymat	7838	7855 S	1871	357 Sequenc	Seguence	373 Sequence	875 S	Sequenc	AX34/8// Sequence	AKU80461 Sequence	M33492 Human trypt	പടക്കു	Human	ma.	ta-tr	BC029356 Homo sapi	Homo	Segue	Sednenc	BD211487 Enzymatic	Sequenc	Sednenc	Sequenc		Sequenc	Sedu		Sednenc	Sequenc		S		223 H	508 S	7881 S	7883 \$	6665 Homo	328059 Homo	1852 Homo	380459 Seque	
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ALIGNMENTS

AX347853 771 bp Sequence 20 from Patent WO0198470. AX347853 AX347853.1 GI:18495660 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AX347853 LOCUS

PAT 01-FEB-2002

linear

DNA

Homo sapiens Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS TITLE

#affit,M., Niles,A.L. and Haak-Frendscho,M.
Recombinant proteolytic tryptases, active site mutants thereof, and
methods of making same

01-FEB-2002

PAT

Euteleostomi;

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GEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/note="unnamed protein product"</pre>
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TLTAAACVGPBDVKDLAALKVGJREQHHYYQQDLPVSRIIHPQFYTAGAIGADIALLE
LEEPVKVSSHYHTVLPPASETFPPGMPCWYTGWGDVDDBELPPPFPLKQVKVPING
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100.0%; Pred. No. 2.3e-117;
tive 0; Mismatches 0;
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/note="unnamed protein product"
                                                                                                                                                                                                              xref="REMTREMBL:CAD22420"
   WO 0198470-A 20 27-DEC-2001;
CORPORATION (US)
                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                           /protein_id="CAD22420.1"
/db_xref="GI:18495661"
                                    Location/Qualifiers
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Bryvsshvhtytlppaaserprepempervytgwgdyndberlppppfplkgvyplmenh
ICDAKYHLGAYTGDMLTRDDMLAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSW
GEGCAQPNRPGIYTRVTYYYLDMIHHYVPKKP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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99.5%; Pred. No. 2.6e-116;
live 0; Mismatches 4;
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/note="unnamed protein product"
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/db_xref="taxon:9606"
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/db_xref="GI:18495649"
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Maffitt,M.A., Niles,A.L. and Haak-Frendscho,M.
Enzymatically-active recombinant human .beta.-tryptase and method of making same
Patent: US 6274366-A 4 14-AUG-2001;
Location/Qualifiers
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                                          AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGGAGACGACGTCCGCATC
                                                               AACCACATITGIGACGCAAAATACCACTIGGCGCCTACACGGGGGGACGTCGCCATC
                                                                                                                                                           Greedigaccacargererengeceggaaccegaeggaereargecaggecree
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                                                                                                                      GICCGIGACGACATGCTGTGTGCCGGGAACACCCGGGGGGGCACTCATGCCAGGGCGACTCC
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/wol_type="unassigned DNA"
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                         Topology: Linear; Enzymatically-active recombinant human beta-tryptase and method of making
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Pred. No. 2.6e-116;
0; Mismatches 4;
                                                                                                                          Location/Qualifiers
                                                                                                                                         sc signal 7..753.

Location/Qualifiers

1..771.

Angains-"Hono sapiens"

/mol type="genomic DNA"

/db_xref="taxon:9606"
Strandedness: Single;
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Matches 767; Conservative
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Enzymatically-active recombinant human beta-tryptase and method of
making same.
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Maffitt, M.A., Niles, A.L. and Frendscho, M.H.
Enzymatically-active recombinant human beta-tryptase and method of
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PN JP 2002515254-A/4
PD 28-MAY-2002
PF 29-OCT-1998 JP 200549745
PR 15-MAY-1998 US 09/079970
PR MARK A MAFFITT, ANDREW L NILES, MARY HAAK FRENDSCHO PC CLZNIS/09, COTAC 6/40, C12NI/19, C12NIS/09, C12R1:645), C12NIS/09 (C12NIS/09, C12R1:645), C12NIS/09
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BPNVSSHVHTVTLPPASETPPPGMPCWTGMGDVDNDRRLPPPFPLKQVKVPIMENH
ICDAKYHLGAYTGDDVRIVRDDMLCAGNTREDSCQGDSGGPLVCKVNGTWLQAGVVSW
GEGCAQPNRPGIYTRVTYYLDMIHHYVPKKP"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                              Recombinant proteolytic tryptases, active site mutants thereof, methods of making same methods of making same Patent: WO 0199470-A 5 27-DEC-2001; PROMEGA CORPORATION (US)
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/db_xref="taxon:9606"
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Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same
Patent: WO 0198470-A 22 27-DEC-2001;
PROMEGA CORPORATION (US)
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                                    541 GICCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGAGACTCATGCCAGGGCGACTCC
                                                                                                                                                 GGCGAGGGCTGTGCCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTG
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GTCCGTGACGACATGCTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGGCGACTCC
                                                                                                                   1 GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Recombinant proteolytic tryptases, active site
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PROMEGA CORPORATION (US)
Pred. No. 1.6e-115;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Recombinant proteolytic tryptases, active site mutants thereof, methods of making same
Patent: WO 019470-A 38 27-DEC-2001;
PROMEGA CORPORATION (US)
                                                                                                           CTGGAGCTGGAGCCGGTGAAGGTCTCCAGCCACGCCACACACGGTCACCCTGCCCCT
                                                                                                                                                                                              GGCGAGGCTGTGCCCAACCGGCCTGGCATCTACACCCGTGTCACTACTTG
  AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
                                                                                     CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCT
                                                                                                                                                                      AATGATGAGGGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA
                                                                                                                                                                                                                                                                                                                                        AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTTACACGGGAGGACGACGTCCGCATC
                                                                                                                                                                                                                                                                                                                                                                                <u>AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGTCCGCATC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCGTGACGACATGCTGTGTGCCGGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTGGATCCACCACTATGTCCCCCAAAAAGCCGTGAAAGCGGCGGCCGCCGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX347871 771 bp
Sequence 38 from Patent WO0198470.
AX347871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (human)
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009 900 099 099 720

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PAT 01-FEB-2002

Query Match

source

FEATURES

CDS

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/translation="lekrIvGgQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVL
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                                                                                                                            PAT 01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                               linear
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Recombinant proteolytic tryptases, active s
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                                                                                                                               DNA
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/db_xref="REMTREMBL:CAD22423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methods of making same
Patent: WO 0198470-A 26 27-DEC-2001;
PROMEGA CORPORATION (US)
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                                                                                                                         AX347859 771 bp
Sequence 26 from Patent WO0198470.
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                                                                                                                                                                                                                     AX347859.1 GI:18495666
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                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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GEGCAQPNRPGIYTRVTYYLDMIHHYVPKKP"
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                                                                                                                                                                                     /note="unnamed protein product"
                                                                                  /mol_type="unassigned_DNA"
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                                                                                                                                                                                                                  /codon_start=1
/protein_id="CAD22422.1"
/db_xref="G1:18495665"
                                                            organism="Homo sapiens"
Location/Qualifiers
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/mol_type="unassigned DNA"
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                                                                                         GTCCGTGACGACATGCTGTGTGCCGGGAACACCCGGAGGGACTCATGCCAAGGAGACGCC 600
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Recombinant proteolytic tryptases, active site mutants thereof,
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                                                           GTCCGTGACGACATGCTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCC
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AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
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Patent: WO 0198470-A 40 27-DEC-2001;
PROMEGA CORPORATION (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 40 from Patent WO0198470.
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Maffit, M., Niles, A.L. and Haak-Frendscho, M.
Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same
Patent: WO 0198470-A 42 27-DEC-2001;
PROMEGA CORPORATION (US)
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Icdarytcaaytgddyriydddmlagantredscgddaggelvckyngtwlqarygm
Gegcaqppnppdiytrvtyyldmihhyvpkkp"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="GI:18495683"
/db_xref="REMTREMBL:CAD22431"
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SSHYHTVTLPPASETFPPARCWYTGWGDVDNDERLPPPFPLKÇVKVPIMEHHICDA
KYHLGAYTGDDVR1YRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGC
AQPNRPGIYTRVTYYLDWIHHYVPKKP"
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                                                                                                                                                                                                                                                                                                                                                                   Length 735;
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/note="unnamed protein product"
                                                                                                                                                                                      /protein_id="CAD22424.1"
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/db_xref="REMTREMBL:CAD22424"
of making same
WO 0198470-A 28 27-DEC-2001;
CORPORATION (US)
                                                                                               /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                    organism="Homo sapiens"
                                                    Location/Qualifiers
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                            97.7%; Score 753.4; DB 6; Length 771; 98.6%; Pred. No. 1.8e-114; Indels 0
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DEFINITION

RESULT 13 AX347861

LOCUS

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VERSION KEYWORDS SOURCE

AUTHORS TITLE

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AAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCCATCGTCCGTGACGACATGCTG
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Stevens,R.L.
Mast cell protease that cleaves fibrinogen
Patent: US 5968782-A 15 19-OCT-1999;
Location/Qualifiers
1 1128
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ilarity 98.7%; Pred. No. 8.3e-111;
Conservative 0; Mismatches 10;
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Sequence 15 from patent US 5968782.
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Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same
Patent: WO 0198470-A 44 27-DEC-2001;
PROMEGA CORPORATION (US)
Location/Qualifiers
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                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                          721 GTCCCCAAAAGCCG 735
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Search completed: July 22, 2004, 12:27:24 Job time: 5134 secs

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us-09-598-982-20.rnpb ( '

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 22, 2004, 12:27:31 ; Search time 569 Seconds Run on:

(without alignments) 6623.689 Million cell updates/sec

US-09-598-982-20 771

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Length	1143	1145	828	1081	1081	1081	1081	1081	2662	828	1154	1158	828	1187
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	Result No.	н	2	3	4	2	9	7	8	6	10	11	12	13	14

11,	Sequence 11, Appl Sequence 11, Appl	11,	9	٦	H	15,	15,	21	21	21	21,	2	25	25,	25	Sequence 25, Appl	ų	2242	e 74,	Ŋ	545	19,	19,	139	19,	29,	m	22,	Sequence 1, Appli
813-432	-10-246-3 -10-174-3	-83	09-918-60	US-10-150-813-15	US-10-139-854-15	US-10-131-409-15	7	-10-150-813-	US-10-139-854-21	-40	US-10-150-811-21	US-10-117-323-2	US-10-150-813-25	-854-2	9-2	US-10-150-811-25	US-10-311-955-1	US-09-954-456-2242	US-09-960-706-74	9	-09-87	-10-150-8	US-10-139-854-19	US-10-131-409-19	US-10-150-811-19	US-10-311-035-29	US-10-266-035-3	-10 - 391 - 36	US-10-266-035-1
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37.3	37.3	37.3	35.7	32.7	32.7	32.7	32.7	30.7	30.7	30.7	30.7	30.3	30.0	30.0	30.0	30.0	29.8	28.9	28.9	28.9	28.9	28.8	28.8	28.8	28.8	28.4	26.1	26.1	26.1
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## ALIGNMENTS

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DEPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Garrall, Joseph M.
APPLICANT: Healy, Aileen
APPLICANT: Healy, Aileen
APPLICANT: Healy, Aileen
APPLICANT: Wach, Nadine S.
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906, ITLLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 1306, ITLLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1811, 1847, 1849, ITLLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
TITLE OF INVENTION: 1981, 261, 1246, 270, 1410, 137, 1811, 1811, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 1810, 
                                                 Sequence 47, Application US/10352684A Publication No. US20030215452A1 GENERAL INFORMATION:
US-10-352-684A-47
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No. US20040086875A1

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GENERAL INFORMATION
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PRIOR FILING DATE: 2002-08-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.8%; Score 731; DB 16;
98.0%; Pred. No. 4.4e-193;
live 0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                               , NAME/KEY: CDS
, LOCATION: (6)...(833)
US-10-352-684A-47
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                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                     FEATURE:
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RESULT 2 US-10-287-226-93 ; Sequence 93, Application US/10287226

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Remaining Prior Application data removed - See File Wrapper or PALM.
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APPLICANT: Vernet, Corine A.M.,
APPLICANT: Zerhusen, Bryan D.,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burgess, Catherine E.,
Chart, John S.,
Chaudhuri, Amitabha,
DiPippo, Vincent A.,
Edinger, Shlomit R.,
                                                                                                                                                                                                                                                                                                                            Ort, Tatiana,
Padigaru, Muralidhara,
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SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                               Li, Li,
Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles,
                                                                                                                                                                                                                                                                                                                                                                  Rastelli, Luca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Spaderna, Steven K. Spytek, Kimberley A
APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Perence,
                                                                                                                                                                                                                  Khramtsov, Nikolai,
                                                                                                                                  Ellerman, Karen,
Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
                                                                                                                                                                                                                                                                                                                                                  Patturajan, Meera,
                                                                                                                                                                                                                                                                                                              Ooi, Chean Eng,
                                                                                                                                                                                     Ji, Weizhen,
Kekuda, Ramesh,
                                                                                                                    Eisen, Andrew,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
LOCATION: (8)..(832)
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LENGTH: 1145
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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Taupier, Jr., Raymond J.,
Vernet, Corine A.M.,
Zerhusen, Bryan D.,
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PRIOR FILING DATE: 2001-11-30
                                                                                                                                                Li, Li,
Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
Miller, Charles B.,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                   Padigaru, Muralidhara,
                                                                                                                                                                                                                                                                                                                   Patturajan, Meera,
Rastelli, Iuca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                      Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
Khramtsov, Nikolai,
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                 Ellerman, Karen,
Gangolli, Esha A.
Gorman, Linda,
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Ort, Tatiana,
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(825)
US-10-287-226-91
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LOCATION: (1).
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LENGTH: 828
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                               316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGAAGGTCTCCAGCCACGTCCACGCTCACCCTGCCCCCTCAGAGACCTTCC 455
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                                 94.8%; Score 731; DB 17; Length 1145; 98.7%; Pred. No. 4.4e-193; ive 0; Mismatches 10; Indels 0
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Publication No. US20040086875A1
GENERAL INPORMATION:
APPLICANT: Agee, Michele L.,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Constance,
APPLICANT: Berghs, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chant, John S.,
APPLICANT: Chant, John S.,
APPLICANT: Chanthuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
                                                                      Matches 737; Conservative
                                                    Best Local Similarity
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US-10-287-226-91
US-10-287-226-93
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                                                                                                                                                                                                                                           FRIOR FILING DATE: 2001-11-20

FRIOR PEDICATION NUMBER: 60/334,421

FRIOR PEDICATION NUMBER: 60/354,392

FRIOR PEDICATION NUMBER: 60/360,148

FRIOR PEDICATION NUMBER: 60/360,148

FRIOR FILING DATE: 2002-02-7

FRIOR PEDICATION NUMBER: 60/364,000

FRIOR PEDICATION NUMBER: 60/364,000

FRIOR APPLICATION NUMBER: 60/334,526

FRIOR PELING DATE: 2002-03-03

FRIOR PELING DATE: 2001-11-20

FRIOR APPLICATION NUMBER: 60/334,409

FRIOR PELING DATE: 2002-02-04

FRIOR APPLICATION NUMBER: 60/334,409

FRIOR PELING DATE: 2002-03-03

FRIOR PELING DATE: 2001-11-20

FRIOR FILING DATE: 2001-11-20

FRIOR FILING DATE: 2001-11-20

FRIOR PELING DATE: 2001-11-20

FROM APPLICATION NUMBER: 60/331,641

FRIOR PELING DATE: 2001-11-20

FRIOR PELING DATE: 2001-11-20

FRIOR PELING DATE: 2001-11-20

FROM APPLICATION NUMBER: 60/331,641

FRIOR PELING DATE: 2001-11-20

FROM APPLICATION NUMBER: 60/331,641

FROM APPLICATION NUMBER: 60/331,641
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME STELE REPREBLICES: 21402-480C CURRENT APPLICATION NUMBER: US/10/287,226 CURRENT FILING DATE: 2002-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

94.7%; Score 730.4; DB 17; Length 828;
Best Local Similarity 99.2%; Pred. No. 6.1e-193;
Matches 734; Conservative 0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                        94.2%; Score 726.2; DB 9;
98.3%; Pred. No. 9.3e-192;
live 0; Mismatches 13;
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR PLICATION NUMBER: US/60/235,863
PRIOR PLILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PATENTIN version 3.0
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Best Local Similarity 98.3
Matches 734; Conservative
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-09-960-706-680
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## TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets
## CURRENT APPLICATION NUMBER: US/09/954,456
## CURRENT APPLICATION NUMBER: US/00/23,617
## PRIOR PLILING DATE: 2000-09-18
## PRIOR APPLICATION NUMBER: US/00/234,052
## PRIOR APPLICATION NUMBER: US/00/234,923
## PRIOR APPLICATION NUMBER: US/00/235,134
## PRIOR PELING DATE: 2000-09-25
## PRIOR PELING DATE: 2000-09-25
## PRIOR PELING DATE: 2000-09-26
## PRIOR PELING DATE: 2000-09-27
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                                                                                                                                                               TGCGGGAGCAGCACCTCTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
  Sequence 2126, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: WILLSAWS
APPLICANT: GELZENDERG, William E.
APPLICANT: Gelzenberg, Robert H.
APPLICANT: Gelzenberg, Robert H.
APPLICANT: Gelzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
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     17 GAATCGTCGGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Genbank Accession No. US20030134324A1 M33493
                                                                                                         812
                                                       737 ATGTCCCCAAAAGCCGTGAAGCGGCC 763
                                                                                                      786 ATGTCCCCAAAAGCCGTGAGTCAGGC
                                                                                                                                                                                                                                ; Sequence 427, Application US/09873319A; Publication No. US20030134324A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.3;
Matches 734; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 427
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US-09-873-319-427
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                                                                 APPLICANT: Munger, william E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
TITLE OF INVENTION: Gene Expression Profiles
FILE REPERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT APPLICATION NUMBER: US/023,323
FRIOR APPLICATION NUMBER: 09/223,323
FRIOR APPLICATION NUMBER: 09/223,323
FRIOR APPLICATION NUMBER: 09/873,319
FRIOR APPLICATION NUMBER: 09/873,319
FRIOR APPLICATION NUMBER: US/023,329
FRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
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US-09-960-706-680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cch 94.2%; Score 726.2; DB 10; al Similarity 98.3%; Pred. No. 9.3e-192; 734; Conservative 0; Mismatches 13;
Sequence 680, Application US/09960706
Publication No. US20030134280A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 680
LENGTH: 1081
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Qy         317 CGGTGAAGGTCTCCAGCCACGTCACCGTGCCCCTGCCTCAGAGACCTTCC 376           Db         36 CGGTGAAGGTCTCCAGCCACGTCCACGGTCACCCTGCCCTGCCTCAGAGACCTTCC 425           Qy         377 CCCCGGGGATGCCTGCTGGCTGGGGGCGATGTGGACAATGATGAGCGCTCC 436           Db         426 CCCCGGGGATGCCTGCTGGGTGACGTGGCGGATGTGATGAGGGCTTC 485           Qy         437 CACCGCGGTGTGTGAGGTCACTGGCTGGGGGCATGTGAGGGCTTCC 485           Qy         437 CACCGCCATTTCTTTGAAGGTGATGAGGTCAAAGGAGAAACCAATTGTGAGG 496           Db         486 CACCGCCATTTCTTTGAAGCAGAGAAGTCCCATAATGGAAAACCAATTGTGAGG 545	497 CAPATRCCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCGTGACGACGACGTC 55	0y 617 TGTGGCGGGGGACCCGGGGGGCGCCTGGGGGGGGGGGGG	Query Match         94.2%;         Score 726.2;         DB 10;         Length 1081;           Best Local Similarity         98.3%;         Pred. No. 9.3e-192;         0;         Amarches 734;         0;         Gaps 0;           Qy         17 GAATCGTCGGGGGTCAGGAGCCCCCAGGAGCCACTGGCAGTGAGCTGAGAG 76         0;         10;<
Qy         557 TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGCCCCTGGTGT 616           Db         606 TGTGTGCCGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGCCCCTGGTGT 665           Qy         617 GCAAGGTGAATGGCACCTGGAGGCGTGGTCAGCTGGGGCAAGGCTTGTGCCC 676           Db         666 GCAAGGTGAATGGCACCTGGTGCAGGGGGTGGTCAGCTGGGGCGAGGGCTTGTGCCC 725           Qy         677 AGCCCAACCGGCTGGTGAGTGACTGACTGACTGACTGACT	737 ATGTCCCCAAAAAGCCGTGAAGCGGC 763 	Second Color   Seco	OY 197 TGCGGGAGCACCTCTACTACCAGGACCAGCTGCCGGTCAGCAGGATCATCGTGC 256  Db 246 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTCACCAGGATCATCGTGC 305  Qy 257 ACCCACAGTTCTACACCGCCCAGATCGAGCCTGCTGCAGAGAGATCATCGTGC 316  Db 306 ACCCACAGTTCTACACCGCCCAGATCGGAGCGCTGCTGCTGGAGGAGC 316  Db 306 ACCCACAGTTCTACACCGCCCAGATCGGAGCGACATCGCCTGCTGGAGGAGC 316

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1239 TGTGTGCCGGGAACACCCGGAGGACTCATGCCAGGGGGACTCCGGAGGGCCCCTGGTGT 1298
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                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7472460CB1
PRIOR APPLICATION NUMBER: 60/209,402
PRIOR FILING DATE: 2000-06-01
PRIOR PLLING DATE: 2000-06-13
PRIOR PLLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-17
PRIOR PLLING DATE: 2000-05-17
PRIOR PLLING DATE: 2000-05-11
PRIOR PLLING DATE: 2000-05-14
PRIOR PLLING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
SEG IN NO 27
LENGTH: 2662
                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                                            TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
                                                                                                                                186 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCCCTCAGGGTGCAAC
                                                                                                TGACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
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APPLICANT: HARALIA, April J.A.; PATTERSON, Chandra
APPLICANT: HARALIA, Narinder K.; REARNEY, Liam
APPLICANT: WALIA, Narinder K.; REARNEY, Liam
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Yalda, ELLIOTT, Vicki S.
APPLICANT: AZIMZAI, Yalda, ELLIOTT, Vicki S.
APPLICANT: POLICKY, Jenniel B.; GANCHI, Ameen R.
APPLICANT: FOLICKY, Jennier L.; LU, Dyung Aina M.
APPLICANT: FOLICKY, Jennier L.; LU, Dyung Aina M.
APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: PROTEASES
FILE REFERENT APPLICATION NUMBER: US/10/275,505
CURRENT APPLICATION NUMBER: US/10/275,505
CURRENT FILING DATE: 2002-11-04
PRIOR FILING DATE: 2001-05-04
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Publication No. US20040081961A1
GENERAL INFORMATION:
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APPLICANT: DELEGEANE, Angelo M.;
APPLICANT: HARALIA, April J.A.; P.
APPLICANT: MALIA, Narinder K.;
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: YAO, Monique G.; BAUGH
APPLICANT: AZIMZAI, Yalda; ELLIOT
APPLICANT: AZIMZAI, Yalda; ELLIOT
APPLICANT: POLICKY, Janniel B.; GA
APPLICANT: POLICKY, Janniel B.; GA
APPLICANT: REDDY, Roopa M.; YUE,
APPLICANT: TANG, Y. TOM
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US-10-275-505-27
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437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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                                                                                                                                                                   Query Match 90.8%; Score 700; DB 17; Length 828; Best Local Similarity 96.6%; Pred. No. 1.7e-184; Matches 715; Conservative 0; Mismatches 25; Indels
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Sequence 45, Application US/10352684A
Publication No. US20030215452A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 89
LENGTH: 828
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                  ; LOCATION: (1)..(825)
US-10-287-226-89
                                                                                                    NAME/KEY: CDS
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Matches
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NUMBER OF SEQ ID NOS: 673
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APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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CURRENT APPLICATION NUMBER: US/10/287,226
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Spytek, Kimberley A.,
Taupier, Jr., Raymond J.
Vernet, Corine A.M.,
                                                                                                                                                                 APPLICANT: Agee, Michele L.,
APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Boldog, Ference,
APPLICANT: Burgess, Catherine E.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhur, Amitabha,
APPLICANT: Eigen, Vincent A.,
APPLICANT: Eigen, Andrew,
APPLICANT: Eigen, Andrew,
                                                                                                                   ; Sequence 89, Application US/10287226; Publication No. US20040086875A1; GENERAL INFORMATION:
                                 1419 ArgreeceAAAAAGeegre 1437
   737 ATGTCCCCAAAAAGCCGTG 755
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Malyankar, Uriel M.,
MacDougall, John R.,
Mezes, Peter S.
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Patturajan, Meera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rastelli, Luca,
Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
                                                                                                                                                                                                                                                                                                                                        Ellerman, Karen,
Gangolli, Esha A.,
Gorman, Linda,
Gerlach, Valerie,
Ji, Weizhen,
Kekuda, Ramesh,
Khramtsov, Nikolai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller, Charles E.,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ooi, Chean Eng,
Ort, Tatiana,
                                                                                    RESULT 10
US-10-287-226-89
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APPLICANT:
APPLICANT:
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CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGCGATGTGGACAATGATGAGCCCCTCC 525
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TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
FILE REFERENCE: PA-0045 US
CURRENT APPLICATION NUMBER: US/10/116,802
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,593
PRIOR APPLICATION UNMBER: 60/281,593
NUMBER OF SEQ ID NOS: 519
SOFTWARE: PERL PROGRAM
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OTHER INFORMATION: Incyte ID No: 378633.40
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Publication No. US20030065157A1
GENERAL INFORMATION:
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Best Local Similarity 94.95
Matches 709; Conservative
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ORGANISM: Homo sapiens
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US-10-116-802-240
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LENGTH: 1158
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APPLICANT: Carroll, Joseph M.
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APPLICANT: Weich, Nadine S.
APPLICANT: Weich, Louise
TITLE OF INVENTION: HENATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
TITLE OF INVENTION: HENATOLOGICAL DISORDERS USING 131, 148, 199, 12212,
TITLE OF INVENTION: 15402, 302, 5677, 1410, 137, 1847, 1849,
TITLE OF INVENTION: 15402, 340, 140217, 837, 1761, 8990 OR 13249 MOLECULES
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
CURRENT PEDLICANTON NUMBER: US 60/354,333
PRIOR FILING DATE: 2002-019
PRIOR APPLICANTON NUMBER: US 60/356,268
PRIOR FILING DATE: 2002-04-26
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PRIOR PLICANTON NUMBER: US 60/395,494
PRIOR FILING DATE: 2002-06-06
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                                                         317 CGGIGAAGGICTCCAGCCACGICCACAGGICACCTGCCCCCGGCCTCAGAGACCTTCC 376
                                                                                                                   406 ccercaacarerecagececercacacacarearecreececerecereacareareerice 465
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                                                                                                                                                                                                                                             466 CCCCGGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGATGACCCCTCC 525
                                                                                                                                                                                                                                                                                                             CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496
                                                                                                                                                                                                                                                                                                                                                                   CACCGCCATTTCCCCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 585
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346 ACCCACAGTICTACAICATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 405
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APPLICANT: Alsobrook, John P.,
APPLICANT: Berghs, Constance,
APPLICANT: Borghs, Constance,
APPLICANT: Boldoy, Ference,
APPLICANT: Chant, John S.,
APPLICANT: Chant, John S.,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Chaudhuri, Amitabha,
APPLICANT: Edinger, Shlomit R.,
APPLICANT: Elerman, Karen,
APPLICANT: Gangolli, Esha A.,
APPLICANT: Gargan, Linda,
APPLICANT: Garlach, Valerie,
APPLICANT: Grand, Valerie,
APPLICANT: Rekuda, Ramesh,
APPLICANT: REKUMA, RAMESH,
APPLICANT: REKUMA, REKUMA, RAMESH,
APPLICANT: REKUMA, REKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application US/10287226; Publication No. US20040086875A1; GENERAL INFORMATION:
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Rieger, Daniel K.,
Rothenberg, Mark E.,
Shenoy, Suresh G.,
Spaderna, Steven K.,
Spytek, Kimberley A.,
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MacDougall, John R.,
Mezes, Peter S.
Miller, Charles E.,
Millet, Isabelle,
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Ort, Tatiana,
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                                                                                                                                                HILLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-480C
CURRENT TILING DATE: 2002-11-04
CURRENT FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2002-02-07
PRIOR FILING DATE: 2002-02-07
PRIOR FILING DATE: 2002-02-07
PRIOR FILING DATE: 2002-03-13
PRIOR FILING DATE: 2002-03-13
PRIOR FILING DATE: 2002-03-13
PRIOR FILING DATE: 2001-11-30
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Taupier, Jr., Raymond J.,
Vernet, Corine A.M.,
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96.3%;
                                                                                           Zerhusen, Bryan D.
Zhong, Mei
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Best Local Similarity 96.39
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US-10-287-226-87
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                                                                  CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: DELEGEANE, Angelo M.; LAL, Preeti G.
APPLICANT: HARALIA, April J.A., PATERSON, Chandra
APPLICANT: HARALIA, April J.A., PATERSON, Chandra
APPLICANT: HARALIA, Marinder K.; KERNBY, Liam
APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
APPLICANT: YAO, Jaming: HENNANDEZ, Roberto
APPLICANT: YAO, Jaming: HENNANDEZ, Roberto
APPLICANT: YAO, Jaming: HENNANDEZ, Roberto
APPLICANT: TANG, Y. TOM
TITLE OF INVENTION: PROTESSS
FILE REFERENCE: PI-0085 USN
CURRENT APPLICANTION NUMBER: US/10/275,505
CURRENT FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
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; OTHER INFORMATION: Incyte ID No: 3897384CB1
US-10-275-505-22
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Publication No. US20040081961A1
GENERAL INFORMATION:
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LENGTH: 1187
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Sequence 11, Application US/09813432
Publication No. US20030148485A1
GENERAL INFORMATION:
APPLICANT: Taupier Jr., Raymond J
APPLICANT: Majmuder, Kamud
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Steven K
APPLICANT: Mazes, Peter S
APPLICANT: Wernet, Corine A. M.
ITILE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
FILE REPERENCE: 15966-729
CURRENT APPLICATION NUMBER: US/09/813,432
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GAGTCCACGCCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCACCCCCAGTGGG
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PRIOR APPLICATION NUMBER: 60/190,835
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/190,768
PRIOR PELLOR DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/190,972
PRIOR PELLOR DATE: 2000-03-22
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US-09-813-432-11
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Pred. No. 6.9e-70;
0; Mismatches 271; Indels
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PRIOR APPLICATION NUMBER: 60/191,199
PRIOR FILING DATE: 2000-03-22
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-28
PRIOR PILING DATE: 2000-03-28
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PRIOR PILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-03-31
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62.6%;
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Best Local Similarity 62.6
Matches 469; Conservative
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ORGANISM: Homo sapiens
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Run on:

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Perfect score:

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	27	193.8	25.1	~	4	-09	8

ORGANISM: Homo sapiens FEATURE:

NAME/KEY: misc\_signal

LOCATION: 7..753 FEATURE: NAME/KEY: CDS

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2	TIS-09-907-794A-256	4	1100	15.2	117	45
Sequence 3, Appli	US-09-636-382A-3	4	942	15.9	122.8	44
Sequence 14, Appl	US-09-636-382A-14	4	1171	16.1	124	43
Sequence 2, Appli	US-09-386-629-2	4	1166	16.8	129.2	42
Seguence 1, Appli	US-09-386-629-1	4	1430	17.0	131.2	41
Sequence 262, App	US-09-902-775A-262	4	1378	17.0	131.2	40
Sequence 262, App	US-09-905-125A-262	4	1378	17.0	131.2	39
Sequence 262, App	US-09-907-794A-262	4	1378	17.0	131.2	38
Sequence 28, Appl	US-09-023-942A-28	4	1165	17.0	131.2	37
Sequence 1, Appli	US-09-636-382A-1	4	1154	17.1	132.2	36
Sequence 7, Appli	US-09-386-642-7	4	1169	18.2	140.6	35
8, 7	US-09-386-642-8	4	1142	18.2	140.6	34
2, 4	US-08-978-404B-2	7	2397	18.7	143.8	33
Sequence 29, Appl	US-09-023-942A-29	4	933	19.7	152	32
Sequence 19, Appl	US-08-978-404B-19	~	3757	19.8	153	31
Sequence 13, Appl	US-09-016-366A-13	7	3757	19.8	153	30
Sequence 8, Appli	US-09-387-375-8	4	1130	23.5	181.2	29
Sequence 1, Appli	US-09-387-375-1	4	1613	24.4	187.8	28
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## ALIGNMENTS

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APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Haak-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
                                                                                                                                                                                                                                                                                                                             STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
                                                                                                                                                                                                                AUDRESSEE: Intellectual Property Department STREET: 8000 Excelsior Drive, Suite 401 CITY: Madison STATE: WISCONST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 37,170
REFERRNCE/DOCKET NUMBER: 34506.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 811-2100
                      Sequence 4, Application US/09079970A; Patent No. 6274366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (608) 831-2106
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
US-09-079-970A-4
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Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GECGAGGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTG 720
                                                                                                                                                                                                                                                                                                                                     CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                       CACCCCCAGTGGGTGCTGACCGCCGCGGCGTGCGTGGGACCCGGACGTCAAGGATCTGGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAGGATCATCGTGCACCCCACAGTTCTACACCGCCCAGATCGGAGCGGACCTCGCCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGAGCTGGAGGAGCCGGTGAAGGTCTCCAGCCACGTCCACGGTCACCCTGCCCCCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTTGGGTGAGGCTGGGGGGATGTGGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGATGAGGGCCTCCCACCGCCATTTCCTCTAAAGCAGGTGAAGGTCCCCATAATGGAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCACATTTGTGACGCAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC 540
                                                                                                                                                                                                                                                                                                        CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGACATCGCCCTG 300
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                                                                              Score 764.6; DB 3;
Pred. No. 4.1e-166;
0; Mismatches 4;
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600 Atlantic Avenue
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APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-016-366A-20
; Sequence 20, Application US/09016366A
; Patent No. 5955431
                                                                              99.2%;
                                                                                                                                        Conservative
                                                                              Query Match
Best Local Similarity
Matches 767; Conserv
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STREET: 60
LOCATION:
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US-09-079-970A-4
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98.7%; Pred. No. 2.1e-158;
iive 0; Mismatches 10;
                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: PLUMEY: Blizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 98.78
Watches 737; Conservative
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                                                                                                                                                   COMPUTER READABLE FORM:
STATE: MA
COUNTRY: U.S.A.
7TP: 02210-2211
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TGACCGCCGCGCGCGTGCGTGGGACCCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC 196
                             207 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
                                                                                                                                                                                                   327 ACCCACAGTICTACACCGCCCAGATCGGAGCGGACATCGCCCTGCTGGGAGCTGGAGGAGC
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                                                                                        TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
                                                                                                                               267 TGCGGGGGCGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
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; Sequence 18, Application US/09016366A
; Patent No. 595541
; GENERAL INFORMATION;
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston STATE: MA
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CIASSIFICATION: 530
PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02210-2211
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                                                                                                                               GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTCAGCTCAGCTGGGGCGAAGGCCTGTGCCC 746
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TGTGTGCCGGGACCCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT
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98.7%; Pred. No. 2.1e-158;
ive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08978404B

Patent No. 5968782

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

TITLE OF INVENTION: FIRRINOGEN

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA
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APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                                                                                                                                                                                                                                            737 ATGICCCCAAAAAGCCGIGAAGCGGCC 763
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REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
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COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TYPE: nucleic acid
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Best Local Similarity 98.7
Matches 737; Conservative
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INFORMATION FOR SEQ ID NO:
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US-08-978-404B-15
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05-FEB-1997

FILING DATE:

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TELEPHONE:
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US-08-978-404B-13
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                   RESULT 5
US-08-978-404B-13
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ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                           INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                        TELEFAX: 617-720-2441
                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 TGACCGCCGCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
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                                                                      APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
WUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.8%; Score 731; DB 2; L 98.7%; Pred. No. 2.1e-158; Live 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 25-NOV-97
                                                                                                                                                                                                              Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: B0801/7090 TELECOMMUNICATION INFORMATION:
; Sequence 13, Application US/08978404B; Patent No. 5968782; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DBC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.7
Matches 737; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-720-2441
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ORIGINAL SOURCE:
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                                 CCCCGGGGATGCCGTGCTGGGTCGGCTGGGCGATGTGGACAATGATGATGACGCCTCC 504
                                                                                   CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGC 556
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                                                                                                                                                                                                                                                                      GCAAGGTGAATGGCACCTGCAGGCGGCGTGGTCAGCTGGGGCGAGGGCTGTGCCC 744
                                                                                                                                                                                                                                                                                                                              AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACCACT 804
       CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCTCC
                                                                 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG
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                                                                                                                                                                                                                                                                                                   AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACCT
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APPLICANT: Maffitt, Mark A.
APPLICANT: Niles, Andrew L.
APPLICANT: Hask-Frendscho, Mary
TITLE OF INVENTION: Enzymatically-Active Recombinant Human
TITLE OF EQUENCES:
GORRESPONDENCE ADDRESS:
ADDRESSE: Intellectual Property Department
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUMPRY: U.S.A.

ZIP: 5317-1914

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,970A
FILING DATE:
FLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leone, Joseph T.
REGISTRATION NUMBER: 34506.073
TELEPHONE: (608) 831-2106
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEONGH: 735 base pairs
TYPE: nucleic acid
TYPE: NUCLEIC ASINGLE
                                                                                                                                                                                                                                                                                                                                                            737 ATGTCCCCAAAAGCCGTGAAGCGGCC 763
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Patent No. 6274366
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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US-09-079-970A-1
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                                                                                                                                                                                                                      19 ATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC
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                                                                                                                                                                                Gaps
                                                                                                                                                                             0
                                                                                                                                  Length 735;
                                                                                                                                                                             Indels
                                                                                                                                Score 728.6; DB 3;
Pred. No. 6.8e-158;
0; Mismatches 4;
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Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stewns, Richard L.
APPLICANT: Huang, Chifu
ITILE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
                                                                                                                             Query Match

Best Local Similarity 99.5%;
Matches 731; Conservative
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ORGANISM: Homo sapiens FEATURE:
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                                             CDS
                                      , NAME/KEY:
, LOCATION:
US-09-079-970A-1
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                                                                                                                                                                                                                                    666 gcaaggrgaanggcaccnggcnccaggcgcgcgcgcgcrcagcrggggcgagggcrgrgccc 725
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                      TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGGGACTCCGGAGGGCCCCCTGGTGT
                                                                                           TGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGGCCCCTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINGGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.2%; Score 726.2; DB 2; 98.3%; Pred. No. 2.6e-157; tive 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                               737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763
                                                                                                                                                                                                                                                                                                                                                                                                                              786 ATGTCCCCAAAAGCCGTGAGTCAGGC 812
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REGISTRATION NUMBER: 36,637
REFENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 17, Application US/08978404B
; Patent No. 5968782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1081 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
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Best Local Similarity
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                                                                                                                                                                                                                                                COMPUTER: 1 LEST COMPOSE SOFTWARES SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,366A FILING DATE: January 30, 1998
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA
APPLICATION NUMBER: 60/037,090
FILLING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                     STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
"AMPTER: IBM Compatible
"AMPTER: IBM Compatible
"AMPTER: IBM Compatible
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LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
    NUMBER OF SEQUENCES:
                                                                       STREET: 600 A
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106 GTATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGGGC
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                                                                                                                                                              B0801/7093
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTONERY/ABENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/70
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 720-3500
TELECATION ELIZABED
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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US-09-016-366A-16
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  TCCACGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCACCCCCAGTGGGTGC
                                                                              TGACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
                                                                                                                                                      TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
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| Patent No. 5955431
| GENERAL INFORMATION:
| APPLICANT: Stevens, Richard L. APPLICANT: Huang, Chifu
| TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
| TITLE OF INVENTION: INHIBITORS
| NUMBER OF SEQUENCES: 65
| CORRESPENDENCE ADDRESS: 3 ADDRESSE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CUREBNY APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTCCCCAAAAGCCGTGAAGCGGCC 763
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677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTTGGACTGGATCCACCACT 736
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317 OGGIGAAGGICICCAGGCCACGICCACACGICACCCTGCCCCTGCCTCAGAGACCTTCC 376
                                                                                                                                                                                                                                                                               CACCGCCATTTCCTCTGAAGCAGGTGGTCCCCATAATGGAAAACCACATTTGTGACG 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGGGGCGAGGGCTGTGCCC
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TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: PIBRINGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           826 Argrecechahahdecerehagreageeregerer 860
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FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/08978404B
; Patent No. 5568782
; GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/032,354
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REFERENCE/DOCKET NUMBER: B01
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TELEPHONE: 617-720-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1219 base pairs
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskett
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SOFTWARE: FastSEC
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                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: FIBRINGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.0%; Score 686.2; DB 2; 94.3%; Pred. No. 3.7e-148; ive 0; Mismatches 43;
                                                                     826 ATGTCCCCAAAAGCCGTGAGTCAGGCCTGGGTGT 860
       737 ATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPETATION SYSTEM: DOS CORRELAGE SYSTEM: DOS CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION 1. 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                  Sequence 11, Application US/08978404B
Patent No. 5968782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-720-2441
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Matches 712; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 02210-2211
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US-08-978-404B-11
                                                                                                                                                                                RESULT 10
US-08-978-404B-11
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LENGTH: 1108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 77.23
Matches 571; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                     GAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGCTCCCTCATCCACCC 125
                                                                                                                                                                                                             GAGCCTTCGTGCCAATGAAACCTACTGGAGGCATTTCTGCGGGGGGCTCCCTCATCCACCC 379
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                                                                                                                                                                                                                                                                       380 ACAGTGGGTGCTCACCGGGGACACTGTGTGGGACCGACTATTGCTGATCCCAACAAGGT 439
                                                                                                                                                                                                                                                                                                                               GCTGGAGGAGCCGGTGAAGGTCTCCAGGCCACGTCCACGGTCACCCTGCCCCTGCCTC 365
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                                                                   61.9%; Score 477.2; DB 2; Length 1219; 77.1%; Pred. No. 2.2e-100; Live 0; Mismatches 173; Indels 0;
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Patent No. 5955431
GENERAL INFORMATION: Richard L.
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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                                                                                               Matches 581; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                   Similarity
                            TOPOLOGY: linear
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US-09-016-366A-14
                                        US-08-978-404B-7
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                                                                                                       COMPUTER: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONS: 617-720-3500
                         STREET: 600 Atlantic Avenue CIIY: Boston
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Db	OY 197 TGCGGGAGCACCTCTACTACCAGGACCAGCTGCTGCGGGTCAGGATCATGGTGC 256  Db 305 TTCGTGAGCAGTATCTATACTATGGGGACCAGCTCCTCTTTGAACCGGATCGTGGTGC 364	QY         257 ACCCACAGITCIACACCGCCCAGAICGGAGCGGACAICGCCTGCTGGAGCTGGAGGAGC         316           Db         365 ACCCCCACIAITACACGGCCGAGGGGGGGGGCAGACGTTGCCCTGCTGGAGCTTGAGGTC         424	QY         317 CGGTGAAGGTCTCCAGCCACGTCCACCCTGCCCTCAGAGACCTTCC 376           Db         425 CTGTGAATGTCTCCACCCATATCCACCCCATATCCTGCCCCTGCCTCGGAGACCTTCC 484	m nate result to a merce of the
Db   605   GGAAGTACCACACTGGCCTCTACACGGGAGATGATTTCCCATTGTCCATGATGCATGC	Qy 617 GCAAGGTGAATGGCACCTGGCTGCGGGCGTGGTCAGCTGGGGCGAGGCTTGTGCCC 676	OY 677 AGCCCAACCGGCTGGCATCTACACCCGTGTCACTACTACTTGGACTGGATCCACCACT 736	OY 737 ATGTCCCGAAAAGCCGTGA 756  Db 845 ATGTCCTGAGCATTCCTGA 864	RESULT 13 US-08-978-4048-20 1 Sequence 20, Application US/08978404B 1 Sequence 20, Seg782 1 General INPORMATION: 1 Factor INPORTION: 2 Factor INPORMATION: 3 FAPILICATION: 3 FAPILICATION: 3 FAPILICATION: 3 FAPILICATION: 3 FAPILICATION: 3 FAPILICATION: 4 FAPILICATION: 4 FAPILICATION: 5 F

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ADDRESSEE:
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77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCACCCCCAGTGGGTGC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 TIAAATTCAGCTTCTGGATGCATTTCTGTGGCGGCTCCCTCATTCACCCACAGTGGGTGC 221
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                                                                                                                               TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE TITLE OF INVENTION: INHIBITORS NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NAME: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION NUMBER: US/09/016,366A
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING APPLICATION NUMBER: 60/037,090
FILING DATE: DOS-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: PLUMEr, Blizabeth R.
REGISTRATION NUMBER: 36,637
REFFERATION NUMBER: 36,637
REFFERATION NUMBER: B0801/7093
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                E: Wolf, Greenfield & Sacks, 600 Atlantic Avenue
Sequence 24, Application US/09016366A Patent No. 5955431 GENERAL INFORMATION:
                                                                               APPLICANT: Stevens, Richard L. APPLICANT: Huang, Chifu
                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.11
Matches 556; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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402 CTGTGAATGTCTCCACCATATCCACCCACACTCCCTGCCCCTGCCTG	377 CCCCGGGGATGCCGTGCTGGGTCACTGGGCGATGTGGACAAAGAAGAGGCGCTCC 436	462 CCTCGGGGACTTCTTGCTGGGTACAGGCTGGGGCGACATTGATAGTGACGAGCCTCTCC 521	437 CACCGCCATTCCTCTGAAGCTGAAGGTCCCCATAATGGAAAACCACATTTGTGACG 496	522 TGCCACCTTATCCTCTGAAGCAAGTGAAGGTCCCCATTGTGGAAAACAGCCTGTGTGATC 581	497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCGACGACGACGTGC 556	582 GGAAGTACCACACTGGCCTCTACACAGGAGATGATGCTTCCCATTGTCCAGGATGGCATGC 641	557 TGTGTGCGGGAACACCCGGAGGACTCATGCCAGGGGACTCCGGAGGGCCCCTGGTGT 616	642 TGTGTGTGGAAAATACCAGGAGGGACTCCTGCCAGGGAGACTCAGGGGGCCCACTGGTCT 701	617 GCAAGGTGAATGGCACCTGCTGCAGGGGGGGTGATCAGCTGGGGGGGAGGGCTGTGCCC 676	702 GCAAAGGGAAGGGTACCTGGCTGCAAGGAGTGGTCAGCTGGGGGCGAGGGCTGCGCAG 761	677 AGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTACTAGACTGGATCCACCACT 736	762 AGGCCAATCGTCCTGGCATTTACACCCGGGTGACGTACTACTGGGATTGACGTGGATTCACCGGTT 821	737 AIGICCCCAAAAAGCCGIGA 756	822 ATGTCCTCAGCGTTCCTGA 841
qq	Š	qq	δλ	qa	ζō	qa	λζ	qu	δδ	qq	δλ	qq	à	qu

Search completed: July 22, 2004, 13:26:09 Job time: 93 secs

us-09-598-982-20.rng

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Copyright

Run on:

US-09-598-982-20

July 22, 2004, 09:37:10; Search time 522 Seconds (without alignments) 6274.637 Million cell updates/sec

Title: Perfect score:

1 gggcccctcgagaaaagaat......cgtgaagcggccgccgtcgt 771 Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

6747726 Total number of hits satisfying chosen parameters:

3373863 segs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_29Jan04:\* Database

genesequ1990s:\*
genesequ2000s:\*
genesequ2001as:\*
genesequ2001bs:\*
genesequ2002as:\*
genesequ2003as:\* geneseqn1980s:\*

geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. score

## SUMMARIES

•	Description	Aas20775 DNA encod	DNA		Ŋ	Aas20763 DNA encod	Aas20776 DNA encod	4 DNA		Aas20777 DNA encod	6 DNA	DNA	Aas20779 DNA encod	DNA	) Huma		Aav44329 Human mas	Aav42711 Human mas	Aaa34957 Human ade		Abz96773 Human nuc	Aaa34955 Human ade	Human	Abz96771 Human nuc
COLUMNIC	ID	AAS20775	AAS20783	AAZ40175	AAS20765	AAS20763	AAS20776	AAS20784	AAS20778	AAS20777	AAS20786	AAS20785	AAS20779	AAS20787	AAV44330	AAV42712	AAV44329	AAV42711	AAA34957	AAF21079	ABZ96773	AAA34955	AAF21077	AB296771
	DB	9	9	٣	9	9	ø	9	9	9	9	9	9	9	~	7	7	~	m	m	7	m	m	7
	Length	771	771	771	771	771	771	771	771	771	171	771	735	735	1128	1128	1137	1137	1137	1137	1137	1143	1143	1143
æ	ery	100.0	8.66	99.5	99.2	0.66	98.8	98.5	97.9	97.9	7.76	7.76	95.3	95.1	94.8	94.8		94.8	94.8	٠	94.8	94.8	94.8	94.8
	Score	771	769.4	764.6	764.6	763	761.4	759.8	755	755	753.4	753.4	735	733.4	731	731	731	731	731	731	731	731	731	731
	Result No.	н	7	33	4	ιŋ	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Aaa34956 Human ade	Aaf21078 Human low	Abz96772 Human nuc	Aaa34962 Human ade	Aaf21084 Human low	Abz96778 Human nuc	Aaz40172 Human bet	Aas20766 DNA encod	Aas20760 DNA encod	Aav44331 Human mas	Aav42713 Human mas	Aaa34960 Human ade	Aaf21082 Human low	Abl62377 Colon ade	Abl66816 Lung canc	Abl61818 Colon ade	Abk35580 Gene TPS2	Abk64532 Human ben	Abz96776 Human nuc	Aas20780 DNA encod	Aas20788 DNA encod	Aas20782 DNA encod
AAA34956	AAF21078	ABZ96772	AAA34962	AAF21084	ABZ96778	AAZ40172	AAS20766	AAS20760	AAV44331	AAV42713	AAA34960	AAF21082	ABL62377	ABL66816	ABL61818	ABK35580	ABK64532	ABZ96776	AAS20780	AAS20788	AAS20782
м	m	7	e	m	7	m	9	9	7	7	m	m	9	9	9	9	9	7	و	9	9
1145	1145	1145	17133	17133	17133	735	735	735	1081	1081	1081	1081	1081	1081	1081	1081	1081	1081	735	735	735
94.8	94.8	94.8	94.8	94.8	94.8	94.5	94.5	94.3	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.1	93.9	93.3
731	731	731	731	731	731	728.6	728.6	727	726.2	726.2	726.2	726.2	726.2	726.2	726.2	726.2	726.2	726.2	725.4	723.8	719
24	25	26	27	28	29		31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 AAS20775

BP AAS20775 standard; DNA; 771

AAS20775;

09-APR-2002

(first entry)

Human; proteolytic tryptase; protease; recombinant beta-II tryptase; enzyme; mutant; ds.

DNA encoding human beta-II tryptase active site mutant H44A #1.

Homo sapiens.

Synthetic.

WO200198470-A2.

27-DEC-2001. 

20-JUN-2001; 2001WO-US019681.

21-JUN-2000; 2000US-00598982.

(PROM-) PROMEGA CORP

Haak-Frendscho Maffit M, Niles AL,

Σ

WPI; 2002-114578/15. P-PSDB; AAU12009. DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.

Claim 7; Page 83-84; 126pp; English.

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a NAA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The

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active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to openerate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS207775-AAS20790 encode for recombinant human beta-II tryptase active
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                                                                                                                                                                                 Length 771;
                                                                                                                                                  Sequence 771 BP; 147 A; 256 C; 244 G; 124 T; 0 U; 0 Other;
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The active site mutants of producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, croembinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC
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                                                                                               DNA encoding human beta-II tryptase active site mutant H44A
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Pred. No. 2.8e-147;
0; Mismatches 1;
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P-PSDB; AAU12017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta-tryptase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant human beta-tryptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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This sequence encodes the human beta-tryptase. The invention relates to

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DNA expression construct comprising (5' to 3') a promoter linked to a signal sequence which is linked to a sequence encoding human beta-tryptase. The DNA construct is useful for transforming host cells to express, post translationally process and secrete enzymatically active human tryptase. The method is useful for the production of large amounts of tryptase with defined specifications. The transformant is useful for pharmacological studies, combinatorial library screens and X ray crystallographic studies. The tryptase produced allows for the acvelopment of tryptase agonists and/or antagonists, is useful as an antagonists, as useful as an antagonists, agonists etc. and to assay for the presence of tryptase in antagonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, agonists etc. and to assay for the presence of tryptase in biological or other solutions. Tryptase inhibitors, antagonists, and initiate tryptase activity and it has enzymatic activity which compares favourably with cadaveric tryptase. The availability of enzymatically continued for specific tryptase scale screening of combinatorial libraries for specific tryptase inhibitors as potential therapeutics and advances the understanding of the biological significance of tryptase in and advances the understanding of the biological significance of tryptase in and advances the understanding of the biological significance of tryptase in
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99.5%; Pred. No. 2.6e-146;
cive 0; Mismatches 4;
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing chase. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase that lacks enzymatic activity due to the a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its encompliant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase produced are useful as an antigen to generate anti-human tryptase antibitors, antagonists, agonists, etc.

The present sequence encodes for recombinant human beta-II tryptase
                  GGCGAGGGCTGTGCCCCAGCCCAACCGGCCTGGCATCTACACCCCTGTCTACTACTTC 720
661 GGCGAGGCTGTGCCCAGCCCAACCGGCCTGGCAICTACACCCGTGTCACCTACTACTTG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active
                                                                                                                                                                                                                                                                                                          Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
enzyme; gene; mutant; ds.
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                                                                                 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
                                                                GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT
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/product= "Recombinant beta-II tryptase"
/note= "This sequence lacks a start codon"
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                                                                                                                                                                                                                                                                         recombinant human beta-II tryptase.
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                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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P-PSDB; AAU12007.
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Score 764.6; DB 6; Length 771;

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Query Match

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                   4.
   Pred. No. 2.6e-146;
                 0; Mismatches
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/*tag= a
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99.5%;
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 Best Local Similarity 99.5
Matches 767; Conservative
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The present sequence encodes for human beta-I tryptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGG 60
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             /product= "Beta-I tryptase"
/note= "This sequence lacks a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 771;
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99.4%; Pred. No. 5.6e-146;
live 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                      Disclosure; Page 72-74; 126pp; English.
                                                                                                       20-JUN-2001; 2001WO-US019681.
                                                                                                                                   21-JUN-2000; 2000US-00598982
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                                                                                                                                                         AATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAA
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Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
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(first entry)

09-APR-2002

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method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to compounds which act as tryptase antibodies and indus screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
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                                                                                                                                                                                           Length 771;
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                                                                                                                                                            Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 U; 0 Other;
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                                                                                                                                                                                             Score 761.4; DB 6;
Pred. No. 1.2e-145;
                                                                                                                                                                                                                             0; Mismatches
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a box sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its tecombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc.

AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
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                                                                                           Human; proteolytic tryptase; protease; recombinant beta-II tryptase; enzyme; mutant; ds.
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                                                           DNA encoding human beta-II tryptase active site mutant D91A
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Pred. No. 2.5e-145;
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99.1%;
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Matches 764; Conservative
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AAS20784 standard; DNA; 771

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RESULT 7

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           241 AGCAGGATCATCGTGCACCCACAGTTCTACACCGCCCAGATCGGAGCGGCAATCGCCCTG
                                                                                             AACCACATTTGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
                                                                                                                                                                                                                                                                                                                                          GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding human beta-II tryptase active site mutant S194A #2.
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P-PSDB; AAU12012.
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DNA construct for producing enzymatically-inactive proteclytic tryptase, comprises DNA sequence encoding proteclytic tryptase having an active site mutation.

Claim 7; Page 91-92; 126pp; English.

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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing active site mutants of these tryptases and the methods for producing comprising a promoter operably linked to a secretion signal sequence which is operably linked to a secretion signal sequence tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase produced are useful as an antigen to generate anti-human tryptase inlibitors, antagonists, agonists, etc.

ANSIONTS-AASION90 encode for recombinant human beta-II tryptase active
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                                                                                                                                                                                                                                                                                                                                                           Sequence 771 BP; 152 A; 255 C; 241 G; 123 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           site mutants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGGTCCCCTCATC
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                                                                                                                                                                                                                                                                                                                     Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
                                      GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 771
                                                                                                                                                                                                                                                                             DNA encoding human beta-II tryptase active site mutant S194A #1.
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                                                                                                                                                 AAS20777 standard; DNA; 771 BP
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DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation. Claim 7; Page 113-114; 126pp; English. WPI; 2002-114578/15. P-PSDB; AAU12020.

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic cryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutants of proteolytic tryptase provide a tool to investigate active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its croombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc.

Sequence 771 BP; 152 A; 256 C; 240 G; 123 T; 0 U; 0 Other;

CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120 CAGGTGAGCCTGAGAGTCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATC 120 cacccccadidesidericaccecades caristerios de carcados de caracterios de caracterio GGGCCCCTCGAGAAAGAATCGTCGGGGTCAGGAGCCCCCCAGGAGCAAGTGGCCCTGG 60 GGGCCCCTCGAGAAAGAATCGTCGGGGGTCAGGAGGCCCCCCAGGAGCAAGTGGCCCTGG CACCCCCAGTGGTGCTGACCGCCGCGGGGTGCGGACCGGACGTCAAGGATCTGGCC Gaps 97.7%; Score 753.4; DB 6; Length 771; 98.6%; Pred. No. 5e-144; ive 0; Mismatches 11; Indels 0 Conservative Similarity 160; 61 61 121 121 181 181 Query Match Local Matches g 셤 ð  $\overset{\sim}{\circ}$ à g

GCCCTCAGGGTGCAACTGCGGGAGCAGCTCTACTACCAGGACCAGGTGCTGCTGCTGCTC 240 GCCCTCAGGGTGCAACTGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTC 240 241

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720 720 661 GecgAgggcrgrgcccAgcccAAccggccrgcArcracacccgrgrcAccracaccrac 771 721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTGT 721 GACTGGATCCACCACTATGTCCCCAAAAAGCCGTGAAGCGGCCGCCGTCGT 661 RESULT 11 d à g à Db

AAS20785 standard; DNA; 771

AAS20785;

09-APR-2002 (first entry)

DNA encoding human beta-II tryptase active site mutant S194A #5.

Human; proteolytic tryptase; protease; recombinant beta-II tryptase; enzyme; mutant; ds.

Homo sapiens. Synthetic.

WO200198470-A2. 

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20-JUN-2001; 2001WO-US019681,

21-JUN-2000; 2000US-00598982

(PROM-) PROMEGA CORP

Ξ Haak-Frendscho Maffit M, Niles AL,

WPI; 2002-114578/15 P-PSDB; AAU12019

180

DNA construct for producing enzymatically-inactive proteolytic tryptase,

comprises DNA sequence encoding proteolytic tryptase having an active

Claim 7; Page 110-111; 126pp; English.

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II tryptase active site mutants

Sequence 771 BP; 150 A; 256 C; 240 G; 125 T; 0 U; 0 Other;

Length 771; Score 753.4; DB 6; Pred. No. 5e-144; 97.7%; Query Match Best Local Similarity

DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active

Example 1c; Page 94-95; 126pp; English.

site mutation.

Haak-Frendscho M;

Maffit M, Niles AL, (PROM-) PROMEGA CORP

WPI; 2002-114578/15 P-PSDB; AAU12013.

20-JUN-2001; 2001WO-US019681 21-JUN-2000; 2000US-00598982

27-DEC-2001

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Human, proteolytic tryptase, protease, recombinant beta-II tryptase, enzyme, mutant, ds. DNA encoding human beta-II tryptase active site mutant H44A #2. AAS20779 standard; DNA; 735 (first entry) Homo sapiens. Synthetic. 09-APR-2002 AAS20779 AAS20779 

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a mature protectly tryptese that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of protecolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant protecolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antegonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
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generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II tryptase active

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                                                                                                                             Gaps
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                                                                                                 Length 735;
                                                                    Sequence 735 BP; 139 A; 246 C; 230 G; 120 T; 0 U; 0 Other;
                                                                                                                             Indels
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                                                                                                 DB 6;
                                                                                               Query Match
95.1%; Score 733.4; DB 6;
Best Local Similarity 99.9%; Pred. No. 5.8e-140;
Matches 734; Conservative 0; Mismatches 1;
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The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks engymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to

Example 1c; Page 115-117; 126pp; English.

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ACCCACAGITCIACACCGCCCAGAICGGAGCGACAICGCCCTGCTGGAGCTGGAGGAGC 386
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                                                                                                                                                                                     CCCCGGGGATGCCGTGCTGGGTCACTGGGTGGGACGATGTGGACAATGATGAGCCCTCC
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                                                                  CGGTGAAGGTCTCCAGCCACGTCACGGTCACCCTGCCCCCTGCCTCCAGAGACCTTCC
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/note= "the start codon is not indicated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This nucleotide sequence includes a coding region for human mast cell tryptase II/beta (see AAW64240). The invention provides: compositions comprising an isolated tryptase-7 that may include chimeric proteins that contain (a) a human tryptase for all but the active site region and (b) the substrate-binding pocket of mouse tryptase-7 or its homologues (see AAW64233-39); a method for treating a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product, to decrease fibrinogen activity; a nucleic acid encoding a serine protease (SP); and a method of producing a mature SP by expressing the inactive zymagen in a host cell, and cleaving the enteroxinase susceptibility domain. The tryptase-7 polypeptides can be used to treat disorders mediated by undesirable thrombus clot formation such as converted at interaction and reocclusion following angioplasty of blood clots associated with pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal vein and peripheral arterial thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGGGAGCAGCACCTCTACTACCAGACCAGCTGCCGGTCAGCAGGATCATCGTGC 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compositions containing tryptase-7, e.g. mouse mast cell protease-7 are used to treat clot formation in e.g. myocardial infarction, reocclusion following angioplasty or pulmonary thrombo-embolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG
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                     Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7; blood clot; anticoagulant; myocardial infarction; reocclusion; thromboembolism; cerebral embolism; thrombosis; therapy; ss.
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Pred. No. 1.8e-139;
0; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 U; 0 Other;
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 66; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (BGHM ) BRIGHAM & WOMENS HOSPITAL.
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Local Similarity 98.7%;
Les 737; Conservative
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                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                     WO9824886-A1
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Matches
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P-PSDB; AAW63175

This cDNA encodes the human mast cell tryptase II/beta which is a homologue of the mouse mast cell protease (mMCP-6) zymogen. The invention provides sequences shown in AAM63160 to AAM63169 that are inhibitors of mMCP-6. These peptides which are tryptase-6 complex inhibitors, can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, urticaria and antioedema, eczematous dermatitis (atopic dermatitis), anaphylaxis, hyperproliferative skin disease, pepticulors, inflammatory bowel disorder, hyperresponsiveness and inflammatory Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated inflammatory disorders e.g. asthma. Disclosure; Page 47-48; 69pp; English skin conditions 

Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 U; 0 Other;

Gaps 0 Length 1128; 10; Indels Score 731; DB 2; I Pred. No. 1.8e-139; 0; Mismatches 10; 94.8%; 98.7%; Local Similarity 98.7 1es 737; Conservative Query Match Matches ò

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TCCACGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCACCCCCAGTGGGTGC 206 TGACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCCCCTCAGGGTGCAAC 196 

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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July 22, 2004, 10:45:20 ; Search time 3404 Seconds (without alignments) 6763.731 Million cell updates/sec Run on:

US-09-598-982-20

Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\* Database :

em\_estba:\*
em\_esthum:\*
em\_estrun:\*
em\_estrun:\*
em\_estpl:\*
em\_estpl:\*
em\_estpl:\*
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gb\_est1:\*
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em\_gss\_inv:\*
em\_gss\_pln:\*
em\_gss\_vrt:\*
em\_gss\_fun:\* mam:\* mus:\* hum:\* em gss 15: 16: 17: 18: 19: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssI:\* gb\_gss2:\*

em gss pro:\* em gss rod:\*

SUMMARIES

		Description		BM919268 AGENCOTRT	BII071733 im3220	BOSSESS THESE STATES THE BOSSESS TO BE SEEN TO SEE THE BOSSESS TO SE THE BOSSESS TO SEE THE BOSSESS TO SE THE BOSSESS TO SEE TH		CDP/T82T Idn/dIT.Y
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## ALIGNMENTS

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University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt information, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."
                                                                                                                                                                               BU071733 589 bp mRNA linear EST 27-AUG-2002
im33a09.yl Human insulinoma Homo sapiens CDNA clone IMAGE:6036761
5' similar to SW:TRYB_HUMAN P20231 BETA-TRYPTASE PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 ACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGCACCCCACAGTTCTACACCGCCC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 Accadeaccaderrecreereaccadearcarcarecreeacaccacacrerrecracaededed 124
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1 (bases 1 to 589)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Bidocrine Pancreas Consortium
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Perrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone placase contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
841 CTATGTCCCCAAAAGCCGTGAGTCCANGGCC 872
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/db_xref="taxon:9606"
/clone="IMAGE:6036761"
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Fax: 617-495-8557
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//Actione lib="NIH MGC 120"
//Actione lib="Organ: pooled pancreas and spleen; Vector:
//Actione lib="Organ: pooled pancreas and spleen; Vector:
//Actione lib="Organ: pooled pancreas from 28 youngle.
//Actione library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 676.2; DB 12; Length 1030;
Pred. No. 1.7e-115;
0; Mismatches 39; Indels 2;
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                                                                                       organism="Homo sapiens"
                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:5748499"
           Location/Qualifiers
                                                                                                                                                                                                                                           /lab host="DH10B"
                                                                                                                           type="mRNA"
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94.58;
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AGENCOURT 8477973 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6196776 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3605 row: m column: 01
High quality sequence stop: 587.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                  365 ACAGGGGAGACGACGTCCGCATCGTCGTCACGACATGCTGTGTGCCGGGAACACCCGGA
                                                                                                                                                                                                                                                                                                                                                   AGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGCCGGTGAAGGTCTCCAGCCACG
                                                                                    TCACTGGCCGATGTGGACAATGATGAGGCGCCTCCCACCGCCATTTCCTCTGAAGC
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                                                                                                                                                                                                                                                             518 ACACGGGAGACGACGTCCGCATCGTCCGTGACGACATGCTGTGTGCCGGGAACACCCCGGA
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                                                               TCCACACGGTCACCTGCCCCTGCCTCAGAGACCTTCCCCCCGGGGATGCCGTGCTGGG
                                                                                                                                                  245 TCACTGGCTGGGGCGATGTGGACAATGAGCGCCTCCCACCGCCATTTCCTCTGAAGC
                                                                                                                                                                                               AGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGCCT
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:6196776"
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BQ720404.1 GI:21859301
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1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
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NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGGACCAGGGGTCG-3' and
5'-GACTAGTTCTAGATGGCGAGGGGCGCT(15)-3'. Size selected
                                                                                                                                                                                                                                                                                                                                                        GCATCGTTGGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        158 TCCGCGACCGATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC
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                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                   75.3%; Score 580.2; DB 13; Length 904; 90.1%; Pred. No. 1.1e-97; ative 0; Mismatches 43; Indels 30;
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CD671851 619 bp mRNA linear EST 24-JUN-2003 fg07g11.yl Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone fg07g11 5', mRNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .642
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/dev stage="Adult"
/dev stage="Adult"
/lab_host="BubHiob"
/clone lib="Human Iris cDNA (Normalized): fg"
/clone lib="Human Iris cDNA (Normalized): fg"
/clone lib="Human Iris cDNA (Normalized): fg"
/note="Organ: Bye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclases III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(CD 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/Ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
                                                                                                                                                                                                                           1 (bases 1 to 619)
Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
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                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Seq primer: M13RP1 reverse primer (ABI).
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/db_xref="taxon:9606"
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                                                                                               Homo sapiens (human)
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Fax: 301 496 0078
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Wistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
Mol. Vis. 8 (4), 185-195 (2002)
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hote="Organ: Bys; Vector: pcMVsDNRf6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by Not1. This Not1 digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
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241 TCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGCCCGTGAACA 300
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Plate: 15 row: a column: 06
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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6/331, N1H, Bethssda, MD 20892-2740, USA
18 1 301 402 3452
Fax: 301 496 0078
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/db_xref="taxon:9606"
/clone="fg15a06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/dev stage="Additu"
//dev stage="Additu"
/lab_host="EMDH10B"
/clone lib="Human Iris cDNA (Normalized): fg"
/clone lib="Human Iris cDNA (Normalized): fg"
/note="Organ: Bye; Vector: pCMVSPORT6; A human iris
library (Dx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by Not! This Not! digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(CUt 500) with 41 mg of Bio-RNA and vector blocking
oligonuclectides. The hybridized Bio-RNA/se-circles were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cesteaacetriccaeccacerccacercacetreccieccccreccreaeaeacctrice 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 TCCACGGCCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 ACCCCCAGITCIACACCCCCAGAICGGAGCGGACAICGCCCTGCTGGAGCTGGAGGAGC
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                                                                                                                                                   Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.1%; Score 525; DB 14; 98.2%; Pred. No. 1.8e-87;
                                                                                                                                                                 National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, US
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 08 row: b column: 10
Seq primer: M13RP1 reverse primer (ABI)
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                    Vis. 8 (4), 185-195 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Iris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="fg08b10"
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Matches 531; Conservative
                                                                                                                 Contact: Wistow G
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Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exomuclass III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (C0t 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA se-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                         14; Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                     Score 531.4; DB ]
Pred. No. 1.2e-88;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                               Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD671891.1 GI:32173622
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98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   642
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361 edadeseccenterrecaadergaarescaeerieeriscaeeceseceresidades 420
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21C Frontier Korean EST Project 2001
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plate: 59 row: B column: 11
High quality sequence stop: 502.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Kim YS
Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +82-42-860-4409
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                           CAAAATACCACCTTGGCGCCTACACGGGGGGACGACGTCCGCATCGTCCGTGACGACATGC 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer seguence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neubert, P., Partsch, E., Peters, M.,
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RZPD: INAG998M058M.
RZPDII: I.M.A.G.B. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDIIB No.972)
Http://www.rzpd.de/CloneCatds/cgi-
bin/showLib.pi.cgi/response7libNo-972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by Bento Soares and M.Fatima Bonaldo
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Best Local Similarity 99.2%; Pred. No. 6.8e-86;
Matches 519; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 722)
Ebert, L., Heil, O., Hennig, S., Neuber's Radelof, U., Schneider, D. and Korn, B. Human UnigeneSet - RZPD3
Conpublished (2003)
Contact: Ina Rolfs
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo. 1 (bases 1 to 502) Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. S., Hahn, Y., Oh, J. H. Y., Kim, J. M., Park, H. S., Kim, S. and Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
                                                                                                                                                                                                                                                 Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
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437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTGTGACG 496
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/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
      Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:6128247"
                                                                                                                       Endocrine Pancreas Consortium
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                                                                                                                                                                                                            Tel: 617-495-1812
                                                                                                                                                                                                                                 Fax: 617-495-8557
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IMAGE:6128247
                                                                                                                                                       obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Thaising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTACACCGCCCAGATCGGGGGGGAGCATCGCCTGCTGGAGCTGGAGGTGGAGGTGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGAGAGAAAATACCA
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                               DB 13; Length 502;
                                                                                                                                                                                                                                                                                           64.3%; Score 495.6; DB 13; Length 99.2%; Pred. No. 4.7e-82; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACACCCGGAGGGACTCATGC 588
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                                                                                                                                                                                                                                                                                                                                    498; Conservative
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                                                                                                                                                                                                                                                                                                                  Similarity
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU787772
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(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
Information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Buolid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
                                                                                                                                                                                                                                  Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: parcreas; Vector: pBluescript SK-; Site 1: Xho1; Site 2: EcoRI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
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                                                              Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 TCCACGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCACCCCCAGTGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCCAGTGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 TGACCGCCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 TGACCGCAGCGCACTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCGGGGAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 CCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGGGGATGTGGACAATGATGAGGCGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 TGCGGGAGCACCTCTACTACAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCGGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGGACGATGAGCGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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CF553058

AGENCOURT 15594982 NIH MGC_183 Homo sapiens cDNA clone
IMAGE:30529468 5', mRNA sequence.
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/lab host="NHH MGC 183"
/clone lib="NHH MGC 183"
/note="Organ: Pooled muscle (cardiac and skeletal);
Vector: pGWV-SPORT6.1; Site 1: ECGRV (destroyed); Site_2:
NotI; Library is oligo-dT primed and directionally cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCCTGCCTCAGAGACCTTCC 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            653 GACATICCIGITGIGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGGACTCCGGGAGG 712
                                                                                                                                               353 ACCCACAGTTCTACACCCCCAGATCGGACGGACATCGCCCTGCTGGAGCTGGAGGAGC 412
293 TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: Gapbbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                            473 CCCCGGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACCAATGATGAGGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 CCACGGCATTTCCTTCTGAAGCAGGTTGAAGGTCCCCATAATGGAAAACCACATTTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 CGCAAAATACCACCTTGGCGCCT-ACACGGGAGACG-ACGTCCGCATCGTCCGTGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553 ATGCT----GTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCG-ACTCCGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 806)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .806
/organism="Homo sapiens"
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/clone="IMAGE:30529468"
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High quality sequence stop: 611.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF553058.1 GI:34889892
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JOURNAL
COMMENT
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   504 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGGAAAAACCACATTTGTGACG 563
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1 (bases 1 to 736)
WHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM1521 row: b column: 03
High quality sequence stop: 725.
Location/Qualifiers
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Itsue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4695458"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
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NIH-MGC http://mgc.nci.nih.gov/.
(EccRV site is destroyed upon cloning). Average insert size 1.7\,\cdot Library was constructed by Invitrogen."
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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13586 row: n column: 05
High quality sequence stop: 609.
Location/Qualifiers
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                  2;
                                                                                                                                              DB 14; Length 806;
                                                                                                                                    59.1%; Score 455.6; DB 14; Length 94.0%; Pred. No. 1.5e-74; ive 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAAATACCACCTTGG--CGCCTACACGGGAGACGA 530
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Contact: Robert Strausberg, Ph.D.
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BQ721078.1 GI:21859975
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                                                                                                                                                                                                       485; Conservative
                                                                                                                                       Query Match
Best Local Similarity
Matches 485; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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5'-GACTRGTTCTAGATCGCGAGCGGCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 05-FEB-2003
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                      /close lib="Lupsk: sympathetic trunk" /close lib="Lupsk: sympathetic trunk" /note="Vector: pGMV-SPORT6 (Life Technologies); Site_1: Not1: Site_2: Sall; cDNA made by oligo-dT priming. Directionally closed using the following adaptors: 5'-TCGACCCACGCTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 TGCTGGAGCTGGAGGCCGGTGAAGGTCTCCAGCCACGTCCACGGTCACCCTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 ACAATGATGAGCGCCTCCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCATAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 AAAACCACATITGTGACGCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TCGTCCGTGAGGATGCTGTGTGCCGGGAACACCCCGGAGGGACTCATGCCAGGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGGCGAGGCTGTGCCCAGCCCAACCGGCCTGGCATCTACACCCGTGTCACCTACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.6%; Score 444.4; DB 13; Length 917; 98.5%; Pred. No. 1.9e-72; ive 0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT 11288628 NIH MGC_135 Mus musculus cDNA clone INAGE:30142408 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGACTGGATCCACCACTATGTCCCCCAAAAAGCCGTGAGTCAGGC 466
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                                                                                                                                                                                                                                        /tissue type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                  /clone="IMAGE:6189508"
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                                                                                                                                                                                                sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.53
Matches 459; Conservative
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Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                            BI413250.1 GI:15174173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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  557
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JOURNAL
                                                                                                                                                                                                                                                                       RESULT 14
BI413250
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SOURCE
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                                                                                                                                                                                                                                                                                                                                              //db xref="taxon:1090"
/clone="IMAGE:30142408"
/lab host="mild (phage-resistant)"
/lab host="mild (phage-resistant)"
/clone lib="NHH MGC 115"
/note="Vector: pCMVSport6.1; Site 1: EcoRV; Site 2: NotI;
/note="Vector: pCMVSport6.1; Site 1: EcoRV; Site 2: NotI;
/normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5,
14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA enrichment: .3k bp. Average insert size 1.6k bp.
/Normalization (Cot value): 7.5 kb. Priming sequence:
5'GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)3' Tissue contributed
by. David Rowe. Library constructed by ResGen, Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTGAAGGTCTCCAGCCACGTCCACACGGTCACCCTGCCCCTGCCCTCAGAGACTTCC 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MgC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMO051 row: j column: 17
High quality sequence stop: 681.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GAATCGTCGGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 TCCACGGCCCATACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCCAGTGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TGACCGCCGCGCGCGTGCGTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 TCACTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCCCACAGGTCTTTCCGGGTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGGGAGCAGCACCTCTACTACCAGGACCAGCTGCTGCCGGTCAGCAGGATCATCGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 CAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCGCATCGTCGTGACGACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
  National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.8%; Score 430.6; DB 14; Length 930; 76.7%; Pred. No. 7e-70; ive 0; Mismatches 165; Indels 3;
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                 mol_type="mRNA"
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Best Local S
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Bonaldo, Ph.D. construction (LLNL)

CURA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov column: 23

High quality sequence start: 32

High quality sequence start: 32

High quality sequence stop: 849.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Lu33"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: NotI; Site_2: EcoRI; 1st extrand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5, refired from pooled refired from the Not I - oligo(dT) primer [5, refired from pooled from the Not I - oligo(dT) primer [5, refired from pooled from the Not I - oligo(dT) primer [5, refired from pooled from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not I - oligo(dT) primer [5, refired from the Not
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602986390F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142478 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 GCATCGTGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 132
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1000)
                                                                               617 GCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCAGCTGGG-GCGAGGGCTGTGCC
TGTGTGCCGGGAACACCCGGAGGGACTCATGCCAGGGCGACTCCGGAGGCCCCCTGGTGT
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Bento Soares and M. Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
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/clone="IMAGE:5142478"
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                     Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fmax: 314 286 1810

Fmax: 314 286 1810

Fmax: 314 286 1810

Fmax: 314 286 1810

Impact cone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 894 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 349.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Soares_pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I
Site=2: Eco R1; 1st strand cDNA was primed with a Not Oligo(dT) primer [5'
AACTGGAAGAATTCGCGGCCCCTTTTTTTTTTTTTTTT 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGCCGGTGAAGGTCTCCAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGCCCGTGAACATCTCCCAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GCAGGTGAAGGTCCCCATAATGGAAAACCACATTTGTGACGCAAAATACCACCTTGGCGC
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                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 420.4; DB 9; Length
Pred. No. 4.8e-68;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="GDB:3808485"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:503497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female"
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Best Local Similarity 94.0°
Matches 458; Conservative
         Contact: Wilson RK
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Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W.
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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IMAGE:503497 5' similar to gb:M30038 ALPHA-TRYPTASE PRECURSOR
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AA131142.1 GI:1692796
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